GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

4, 2002, 10:12:27; Search time 29.49 Seconds (without alignments) 741.999 Million cell updates/sec October

US-09-299-139A-1 197 Title: Perfect score: Sequence:

1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

747574 segs, 111073796 residues Searched:

0 Word size :

747574 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:\*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
3: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:\*
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13: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:\*
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22: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1997.DAT:\*

15: 16: 17: 18:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Propionibacterium Novel human diagno Propionibacterium Human tumour necro Human neurofilamen Human lymphotoxin TNF-R extracellula Extracellular doma Human TNF-R extrac TNFR molecule LT-b Description AAY31326 AAW94642 AAB69194 AAU04498 AAB36700 AAY20502 AAU65981 ABG20744 AAU58231 ABG08131 H Length DB 197 197 77 77 38 415 71 71 75 80 94 Query Match Score 77 77 10 10 7

Propionibacterium	Novel human diagno	Novel human diagno	ß	Novel human diagno		is	is	i.S	Arabidopsis thalia	Alpha-amylase-8-C.	Rice alpha-Amy8-C	Rice alpha-amylase	Alpha-amylase rela	C glutamicum prote	Maize 4-coumarate:	Human pif-1 type h	Drosophila melanog	Staphylococcus aur	Myxoma virus immun	Amino acid sequenc	Primer generating	Human complementar	Reactive peptide w	Sequence of synthe	Sequence of synthe	Sequence of synthe	ot	φ	ч.	usec		ĕ	N-terminal peptide
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12	13	14	15	16	17	18	19	20	21	22	. 53	24	25	26	27	28	53	3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human; lymphotoxin beta; receptor; blocking agent; extracellular; ligand binding; domain; treatment; Thl cell; immune response; delayed; hypersensitivity; contact; tuberculin; granulomatous; graft versus host; disease; organ rejection; autoimmune; disorder; multiple sclerosis; insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia; psoriasis; Listeria; Toxoplasma; infection; Mycobacterium; abnormal; lymphoid organ; development. Extracellular domain of human lymphotoxin beta receptor. AAW23220 standard; protein; 197 AA (first entry) 29-0CT-1997 AAW23220; RESULT AAW23220 

Homo sapiens WO9703687-A1 36-FEB-1997

96WO-US12010. 95US-0505606 (BIOJ ) BIOGEN INC. 19-JUL-1996; 21-JUL-1995;

Hochman PS; Benjamin CD, Browning JL,

WPI; 1997-132373/12.

Novel human diagno

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                                                                                                            The present sequence, a human lymphotoxin beta receptor (LT-beta-R) blocking agent, comprises the extracellular ligand binding domain of the human LT-beta-R up to the transmembrane region. It can be used to treat a Thi cell mediated immune response which contributes to a delayed type hypersensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin dependent diabetes, sympathetic conditions exacerbated by the activities of Th-1 type cytokines, or Listeria, Toxoplasma or Mycobacterium infection. Its ability to selectively or partially block the LT-beta-R pathway may be useful; in the treatment of abnormal lymphoid organ development associated with misexpression or overexpression of signalling by the LT-beta-R pathway. The present LT-beta-R blocking agent is capable of salector mechanisms. As Thi Cytokines can inhibit Th2 cell dependent responses, the present LT-beta-R blocking agent may also indirectly stimulate certain Th2 cell dependent responses which are normally inhibited by Th1 induced cytokines. Doses of about 1 mg/Kg of the present soluble LT-beta-R are expected to be suitable starting doses for optimising treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell; immune system; tumour; follicular lymphoma; extracellular domain; human
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comprising lymphotoxin-beta receptor blocking agent auto:immune diseases, e.g. sclerosis,
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                                                                             Example 1; Pages 55-56; 76pp; English.
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                                    insulin-dependent diabetes, etc.
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  Compositions
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administered for altering the survival or maintenance of follicular dendritic cells in a subject and for altering the architecture of the organs of the immune system. The method is useful for treating tumours, specifically follicular lymphomas. It offers an alternative therapy for those with tumours resistant to traditional chemotherapy. The present sequence represents the extracellular region of the human Libeta-receptor and comprises the ligand binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a method for arresting or reducing, severity of effects of a tummour by administration of a composition which inhibits the interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor of the interaction between LT-beta and its receptor can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New method of treating follicular lymphomas by inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interaction between lymphotoxin-beta and its receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 197; DB 20;
Pred. No. 4.2e-200;
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                                                                                                                                                                                                                                                                         Tsiagbe V;
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unknown

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RESULT
AAB36700
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                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pre-ligand assembly domain (PLAD). This protein and others of the TNFR superfamily can be utilised to inhibit PLAD self-association, TNF receptor or Fas oligomerisation in a cell and ligand binding to members of the TNFR superfamily or Fas. The PLAD containing proteins are also useful for treating inflammation associated with autoimmune disease and in screening for inhibitors of PLAD association. The treatable disorders include periodic fever syndromes, sepsis syndromes, adult respiratory distress syndrome, ulcerative colitis, Crohn's disease, rheumatoid arthritis, autoimmune gastritis, psoriasis, Still's disease, Behcet's disease, Sjogren's syndrome, ankylosing spondylitis, autoimmune uveitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           necrosis factor receptor (TNFR) protein pre-ligand assembly domain (PLAD). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease
              anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
gene therapy; restenosis; graft versus host disease; tumour; cancer;
                                         Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory;
                                                                                                                         Human
                                                                                                                                                       15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune lymphoproliferative syndrome multiple sclerosis, pernicious anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A polypeptide comprising the isolated amino acid sequence of a pre-ligand assembly domain (PLAD) of a TNF-like receptor for inhibiting TNF receptor or Fas oligomerisation in a cell and for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lenardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-2000; 2000US-0181909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
 apoptotic
                                                                                                                                                                                  AAB36700;
                                                                                                                                                                                                               AAB36700 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune orchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US
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                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                       CPPGTYVSAKCSRIRDTVC
                                                                                                                                                                                                                                                                                         cppgtyvsakcsrirdtvc
                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US04125
                                                                                                                      necrosis factor receptor LTbR protein SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
10
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                                                                                                                                                                                                               Protein; 415
                                                                                                                                                                                                                                                                                                                                                                  9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myasthenia gravis,
 related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siegel RM
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                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                  Score 19;
Pred. No.
 disease;
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                                                                                                                                                                                                                                                                                                                                                     Mismatches
autoimmune
                                                                                                                                                                                                                                                                                                                                                                 DB 22;
1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodpasture's syndrome, polyendocrinopathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain (CRDI) of the tumour LT-beta-R, which comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALPS),
                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyper IgM syndrome,
                                                                                                                                                                                                                                                                                                                                                                             Length 38
disorder
                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes
                                                                                                                                                                                                                                                                                                                                                    Gaps
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polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autolumnune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The, antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding a TRID polypeptide, also referred to necrosis factor receptor 5, useful in the diagnosis, treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200071150-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                          activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins
                                                                                                                                                                                                                                                                                                         nootropic,
                                                                                                                                                                                                                                                                                                                   intracellular domain, also referred to as tumour necrosis factor receptor 5 (TWFR-5 or TR5)). TRID has cytostatic, immunosuppress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2000
                                                                                                                                                                                                                                                                                          antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
                                                                                                                                                                                                                                                                                                                                                         (TNF) related apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                        (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                        Fig 2; 285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US13515
                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, autoimmune disorders and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,
MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9908-0135164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gentz
                                                                                                                                                                                                                                                                                                                                                                          describes the human TRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.
                                                                                                                                                                                                                                                                                                                                                         inducing ligand
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                                                                                                                                                                                                                                                                                                                                                          (TRAIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment
                                                                                                                                                                                                                                                                                                                                                            receptor without
                                                                                                                                                                                                                                                                                                                                                                          (tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as tumor
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Matches Query Match Best Local Local Similarity 10; Conservative 5.1%; 0; Score 10; Pred. No. Mismatches DB 22; 0.049; 0; Length 415; Indels

0;

Gaps

0

Sequence

ΑĄ;

with TRID 415

in

the exemplification

(b) autoimmune disorders;(c) diseases associated with increased apoptosis;(d) cardiovascular disorders;and(e) viral infection polynucleotides, proteins, antibodies, agonists and antagonists useful in the diagnosis, treatment or prevention of: (a) cancer:

represents a tumour

necrosis factor receptor used

cancer;

and

of the

present

invention

polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The Telescopies

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80

## AAY20502 RESULT 7

AAY20502 standard; Protein; 71

KWW XXX ACX AAY20502;

ID

(first entry)

Human neurofilament-L mutant protein fragment

Alzheimer's Huntington's Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease;

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RESULT
AAB65194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                     osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic; antirheumatic; antiarthritic; antiinflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis;
                              08-FEB-2001
                                                                                                                              periodontal
T cell prol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF. They may be used in treating TNF-associated conditions such as acute and chronic inflammatory
                                                             WO200108699-A1
                                                                                                                                        Paget's disease; metastatic bone disease; rheumatoid arthritis; periodontal disease; modulating dendritic cell maturation;
                                                                                                                                                                                                                                         Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-rich domain of TNF-R from
                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                       Human TNF-R extracellular Cys-rich domain TNF-R-rp SEQ ID
                                                                                                                                                                                                                                                                                                        30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                      AAB69194 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, transplantation rejection and malaria. Administration is, e.g. oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greene MI, Murali R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPE-) UNIV PENNSYLVANIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w compounds designed from a binding loop of a tumour necrosis ctor receptor - are capable of inhibiting the biological tlyities of tumour necrosis factor, e.g., in treating inflammation autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                       4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cthcellsdcppgteae
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                                                                                                                           proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                        (first entry)
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100.0%; Pr
                                                                                                                           CD40
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                                                                                                                                                                                                                                                                                                                                                                        77
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                                                                                                                                                                                                                                                                         NO: 3
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28-JUL-2000; 2000WO-US20510.

Misc-difference

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                    Crohn's disease; autoimmune gastritis; Still's disease; Behcet's disease; Sjogren's syndrome; ankylosing spondylitis; autoimmune uveitis; autoimmune lymphoproliferative syndrome; hyper IgM syndrome; multiple sclerosis; pernicious anaemia; Goodpasture's syndrome; autoimmune orchitis; myasthenia gravis; polyendocrinopathy; thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and immunomodulatory activities, and are tumour necrosis factor (TNF) related activation-induced cytokine (TRANCE)/ receptor activator of NF-kappaB ligand (RANK) inhibitors. The method is useful for treating diseases characterised by bone loss such as osteoporosis, Paget's disease, metastatic bone disease, rheumatoid arthritis or periodontal disease, and modulating dendritic cell maturation, T cell proliferate and/or CD40 receptor systems. The present sequence represents and/or CD40 receptor systems. The present sequence represents actor receptor type of a tumour necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a memory obteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory and are tumour necrosis factor (TMF)
                                                                                                                                                                                     pre-ligand assembly domain; oligomerisation; inflammation; psoriasis;
periodic fever syndrome; sepsis syndrome; ulcerative colitis; ALPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aoki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYPE-)
                                                                                                                                                                                                                                                  TNFR molecule LT-beta-R cysteine-rich domain #1 (CRD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use
for
                                                                                                                                                                      adult respiratory distress syndrome; rheumatoid arthritis;
                                                                                                                                                                                                                     TNFR superfamily; tumour necrosis factor receptor superfamily;
                                                                                                                                                                                                                                                                               24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                             AAU04498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BARO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
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                                                                                                                                                                                                                                                                                                                                                                             ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of peptides and peptide analogs which are {\tt TRANCE/RANK} inhibitors, inhibiting osteoclastogenesis and bone resorption -
                                                                                                                                                                                                                                                                                                                                                                                                                       cthcellsdcppgteae
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,
                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vcatcaensynehwnylticqlcrpcdpvmgleeiapctskrktqcrcqpgmfcaawale
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                                                                                                                                                                                                                                                                                                                                             Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.1%; Score 77; 100.0%; Pred. No.
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                                                                                                                                                                        LT-beta-R;
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This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift caused by, or associated with, an RNA molecule that has a frameshift caused by, or associated voidagnose age-related diseases, especially cancer and a wide range of neurodegementive disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, Cd disease, Down's disease, II is an accorption to the method allows a definitive diagnosis of Alzheimer's disease in living patients, Cd allows a definitive diagnosis of Alzheimer's disease in living patients, Cd allows a definitive diagnosis of Alzheimer's disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including Cd proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule cosociated protein 2 (MAP2), neurofilament-L, neurofilament-M, cd neurofilament (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group cyclein C (HMGP-C) and neuroendocrine specific protein A.
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diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
               ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; preseniln I; preseniln II; cellular tumour antigen; gqlial fibrillary acidic protein; GRAP; p53; semaphorin III; HUFF-I; bcl-2; B-cell leukemia/lymhoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
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100.0%; Pred. No. 16;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                ROYAL NETHERLANDS ACAD ARTS & SCI. UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 7; 258pp; English.
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                                                                                                                                                                                                                                                                                               98WO-IB00705.
                                                                                                                                                                                                                                                                                                                                    97US-0043163.
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                                                                                                                                                                                                                                                                                                                                                                             (UYUT-) RIJKSUNIV UTRECHT.
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Best Local Similarity
'-hac 7; Conserve
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                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burbach JPH,
                                                                                                                                                                                                            WO9845322-A2
                                                                                                                                                                                                                                                                                            02-APR-1998;
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                                                                                                                                               Synthetic
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by constitutions. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies contacting the amount of bound protein in the sample. The comparison and activity of P. acnes polypeptides and therefore treat P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as chagnostic agents for determining P. acnes presence, for example, by cerayme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed contacting the contact of the printed contacting the contact of the 
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                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                       Propionibacterium acnes immunogenic protein #26877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW, Persing DH, Mitcham JL, Wang SS,
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
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100.0%; Pred. No. 17;
tive 0; Mismatches
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                             20-APR-2001; 2001WO-US12865
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                                                                                                                                                                                            Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 51103; 103pp; English.
                          Novel human diagnostic protein #20735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU58231 standard; Protein; 94 AA.
                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                            31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
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                                                                                                                  WO200175067-A2.
                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  biodiversity
                                                                                                                                            11-OCT-2001.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyellits; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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Propionibacterium acnes immunogenic protein #19127
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                                                                                                                                                                                   dermatological; osteopathic; neuroprotectant
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100.0%; Pred. No.
:ive 0; Mismatch
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Zhang Y, Jen S, C
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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Best Local Similarity
Matches 7; Conserv
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WO200181581-A2.
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                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 38490; 103pp; English.
                         Novel human diagnostic protein #8122.
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Best Local Similarity 100.0%; Pi
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                 30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                         2000US-0540217.
2000US-0649167.
 (first entry)
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                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                WO200175067-A2
                                                                                         Homo sapiens.
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23-AUG-2000;
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 13-FEB-2002
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                    SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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Propionibacterium acnes immunogenic protein #11038.
                                                                                                                                                                                   dermatological; osteopathic; neuroprotectant.
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100.0%; Pred. No. 23;
tive 0; Mismatches
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e J, Zhang Y, Jen S, Ca
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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Best Local Similarity
7; Conserve
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32 CSRCPPG 38
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35 csrcppg 41
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                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 32121; 103pp; English.
                           Novel human diagnostic protein #1753.
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23-AUG-2000; 2000US-0649167
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13-FEB-2002 (first entry)
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                                                                                                               WO200175067-A2.
                                                                                        Homo sapiens.
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ABG05157
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) of to treat disease states involving to restore normal activity of (II) of to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating isod supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. Abdolout-Bada30377 represent novel human call sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Novel human diagnostic protein #5148.
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 100.
Matches 7; Conservative
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N-PSDB; AAS69344.
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PR 30-AMC 1999; 9908-015130.
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PR 11-SEP 1999; 9918-015376.
PR 12-SEP 1999; 9918-015376.
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PR 22-SEP 1999; 9918-01546.
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PR 23-SEP 1999; 9918-01556.
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Query Match 3.6%; Score 7; DB 21; Length 211; Best Local Similarity 100.0%; Pred. No. 41; Matches 7; Conservative 0; Mismatches 0; Indels 0;

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Gaps

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Search completed: October 4, 2002, 10:16:32 Job time: 245 sec

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/378,968
FILING DATE: 26-JAN-1995
ATOCNEY/AGENT INFORMATION:

NAME: HALEY, Jr., James F.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B191
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 107596-9000
TELECAX: (212) 596-9000
TELEX: 14 48367
INFORMATION FOR SEQ ID NO: 1:
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TYPE: amino acid
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US-08-505-606-1
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-129-129-6
US-08-45-924-8
US-09-146-950-8
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Sequence Sequence Sequence

> US-08-276-151-4 US-09-146-950-4

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Sequence 1, Application US/08505606
Patent No. 5925351
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
BENJAMIN, Christopher D.
APPLICANT:
APPLICANT:
HOCHMAN, Paula S.
TITLE OF INVENTION:
TITLE OF INVENTION:
THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
TITLE OF INVENTION:
DISEASE
NUMBER OF SEQUENCES:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
James F. Haley, Jr.
                    Sequence 13, Appl Sequence 1, Appl Sequence 1, Appl Sequence 178, App Sequence 178, App Sequence 177, Appl Sequence 178, App Sequence 178, App
                                                                                                                                                                                         Sequence 178, App
Sequence 178, App
Sequence 2, Appl
Sequence 215, App
Sequence 18, App
Sequence 5, Appl
Sequence 5, Appli
Sequence 1, Appli
        Sequence
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,606
FILING DATE: 21-JUL-1995
US-09-146-950-20
US-09-133-41-13
US-09-199-842-1
US-08-906-769-178
US-08-906-769-178
US-08-007-178-178
US-09-004-731-77 US-09-012-431-178
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STATE: New York
COUNTY: U.S.A.
ZIP: 10020
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MEDIUM TYPE: Floppy di
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                                                                                                                                                                                                                     121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
                                        Gaps
                                                                                             1 SQPQAVPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                          1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PEPTIDES AND PEPTIDE
TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
TITLE OF INVENTION: USES
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
                                      ;
0
Length 197;
                                      0; Indels
100.0%; Score 197; DB 2; I
100.0%; Pred. No. 7.8e-198;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009113-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFRAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEN COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAX-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEHERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Mural1, Ramachandran
APPLICANT: Takasaki, Wataru
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08866545 Patent No. 6265535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: No. 6265535e
                                                                                                                                                                                                                                                                                            181 TICKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                               181 TTCKNPLEPLPPEMSGT 197
                   Best Local Similarity 100. Matches 197; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-866-545-3
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   Query Match
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Length 77;

39.1%; Score 77; DB 4; L6 100.0%; Pred. No. 4.9e-73;

Query Match Best Local Similarity

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52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                   Gaps
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Sequence 6, Application US/07973324A

Sequence 6, Application US/07973324A

Sequence 6, Application US/07973324A

Settle No. 5460952

GENERAL INFORMATION:
APPLICANT: Yu, Su-May

APPLICANT: Liv, Li-Pei

TITLE OF INVENTION: Gene Expression System Comprising the TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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100.0%; Pred. No. 0.017;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        APPLICANT: WEI, YING-FEI
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: GUBEN, STEVEN
ITILE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                       E: HUMAN GENOME SCIENCES, INC. 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                              Sequence 6, Application US/09006353A Patent No. 6261801
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36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 415 amino acids TYPE: amino acid
                                                                                   112 CTHCELLSDCPPGTEAE 128
                                                                                                       61 CTHCELLSDCPPGTEAE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 ARCQPHTRCE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 ARCQPHTRCE 194
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OTTY: ROCKVILLE
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROC
STATE: MD
COUNTRY:
                                                                                                                                                                                                             US-09-006-353A-6
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Gaps

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APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Liu, Ming-Tsair
ITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
                                                                                                                                                                                                                                                                                                                                                Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Marshall, O'Toole, Gerstein, Murray
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENY APPLICATION DATA:
RPPLICATION NUMBER: US/09/072,435
FILING DATE:
                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
APTICANION NUMBER: US 07/973,324
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                              3.6%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-00-072-435-6; Sequence 6, Application US/09072435; Patent No. 6215051
                                          REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
                            25447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
                                                                                                             TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein
US-08-343-380-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-072-435-6
                        REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GTEAELK 130
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Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.6%; Score 7; DB 1;
100.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/973,324A FILING DATE: 04-NOV-1992 CLASSIFICATION: 435
                                                                                                      STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/343,380 FILING DATE: 22-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 437 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDAL.
STREET: 0.0.
TTW: Chicago
                                                                                  Chicago
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| 90 GTEAELK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-973-324A-6
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US-08-343-380-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.0
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washir
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TSSPSA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-08-137-016-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                              ;
0
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                                                                                                                                                                                                                                                                                       APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
IIILE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
    Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 4; Length 437;
Pred. No. 24;
                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: 111inois
COUTRY: United States of America
21P: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
Query Match 3.6%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOKNEL CASE, CONTROL A. NAME: Gass, David A. ROALSTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            Sequence 6, Application US/09072917A
Patent No. 6288302
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US-08-137-016-2
; Sequence 2, Application US/08137016
; Patent No. 5494999
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Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-072-917A-6
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Yu, Su
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                                                                                  124 GTEAELK 130
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                                                                                                                          90 GTEAELK 96
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                                                                                                                                                                                                           US-09-072-917A-6
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APPLICANT TONE, Masabide
APPLICANT TONE, Masabide
APPLICANT TONE, Masabide
TITLE OF INVENTION: Synthetic CDM52 (Campath-1) Peptide Antigen
NUMBER OF STOURNES: 14
CORRESONDERCE ADDRESS: 4
CORPUTES: 1816 OF 101 E, 555 Thitteenth St., N.W
STREET: SMILE OF 101 E, 555 Thitteenth St., N.W
CORPUTES: Rotherl, Figg. Ernet & Kutz
1171: Washington
COMPUTES: Rotherl, Prop. Pr
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Gaps

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Sequence 5, Application US/08137016
Patent No. 5494999
GENERAL INFORMATION
APPLICANT: TONE, Masahide
APPLICANT: XIA, Meng-Qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:

U.S.A.

21P: 20004

COUNTRY:
U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 16-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: ELBCAT NUMBER: 30.377
REFERENCE/DOCKET NUMBER: 30.377
REFERENCE/DOCKET NUMBER: 1768-116
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.0%; Score 6; DB 1.
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches
                          REFERENCE/DOCKET NUMBER: 1768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
       30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)783-6031 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
       REGISTRATION NUMBER:
                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 TSSPSA 156
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STATE: D. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TSSPSA 13
                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
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US-08-137-016-4
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US-08-137-016-5
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APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: TONE, Masahide
APPLICANT: TONE, Masahide
APPLICANT: TONE, Masahide
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 14;
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                 CURRENT AFPLICATION DATA:
PRICE APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,377
REFERENCE/COCKET NUMBER: 1768-116
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/GB 92/00705
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 12
Mismatches
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100.0%; Pred. No
:ive 0; Mismat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08137016
Patent No. 5494999
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.0
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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US-08-137-016-3
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Sequence 7, Application US/08137016
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US-07-826-928A-11
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                                                                                                    Gaps
                                                                                                                                                                                                                                                                         Sequence 6, Application US/08137016
Patent No. 5494999
GENERAL INFORMATION
APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: XTA, Meng-Q1
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                           Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SUBTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 05-0CT-0993

PRIOR APPLICATION DATA: WO PCT/GB 92/00705

FILING DATE: 16-APR-1992

PRIOR APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91

APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91

APPLICATION NUMBER: SB 91 08056.4
FILING DATA: 16-APR-91

RESISTATION: NUMBER: 30,377

RESISTATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1768-116

TELECOMMUNICATION INDERS: 1768-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Rothwell, Figg, Ernst & Kurz
Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 14; ive 0; Mismatches
                                                       Query Match 3.0%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                       151 TSSPSA 156
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                                                                                                                                                                              8 TSSPSA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-08-137-016-6
                                                                                                                                                                                                                                      RESULT 12
US-08-137-016-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
US-08-137-016-5
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US-08-137-016-7
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APPLICANT: Kasher, Mary S.

APPLICANT: Smitch, Michele C.
APPLICANT: STERMEN Willem P.

TITLE OF INVENTION: METHOD OF IMMOBILIZING AND CROSS LINKING
TITLE OF INVENTION: PROTEINS AND OTHER MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
APPLICANT: HALE, Geoffrey
APPLICANT: TONE, Masahide
APPLICANT: XIA, Meng-Qi
TITLE OF INVENTION: Synthetic CDW52 (Campath-1) Peptide Antigen
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: U.S.A.

CID: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/137,016
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91 08056.4
FILING DATE: 16-APR-91
RILING DATE: 16-APR-91
RELING DATE: 16-APR-91
RILING DATE: 16-APR-91
RILING DATE: 16-APR-91
RILING DATE: 16-APR-91
RILING DATE: 16-APR-91
RELING DATE: 16-APR-91
RE
                                                                                                                                                                                                                                                                                                                  E: Rothwell, Figg, Ernst & Kurz
Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.0%; Score 6; DB 1;
100.0%; Pred. No. 15;
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Mismatches
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APPLICANT: Cook, James A.
APPLICANT: David, Gary S.
APPLICANT: Hochschwender, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/07826928A Patent No. 5439829 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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Best Local Similarity
Matches 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D. C. COUNTRY: U.S.A.
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0; Gaps

Length 40; 0; Indels

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FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 203424/T7016(C)
TELECHONE: (202) 861-3000
TELEFAX: 6714677CSH
INFORMATION FOR SEQ ID NO: 5SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                              Score 6; DB 1; Pred. No. 31; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: October 4, 2002, 10:16:52 Job time: 220 sec
                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-129-129-6
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserva
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Fatent No. 5767363
GENERAL INFORMATION:
APPLICANT: DE SILVA, Jacqueline
APPLICANT: BAFFORD, Richard
APPLICANT: HGGHES, Stephen Glyn
TITLE OF INVENTION: PLANT PROMOTER INVOLVED IN
TITLE OF INVENTION: CONTROLLING LIPID BIOSYNTHESIS IN SEEDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                 SOFTWARE PATENTIN SISTEM
SOFTWARE PATENTIN BELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/826,928A
FILING DATE: 19920124
CLASSIFICATION: 435
ATOMNEY/AGENT INFORMATION:
NAME: MUTPHY, Richard B.
REGISTRATION NUMBER: 35,296
REBRENCE/POCKET NUMBER: 35,296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-5389
TELEFRAK: 317-276-5389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
WORKENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,129
FILING DATE: 18-JAN-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%; Score 6; DB 1;
100.0%; Pred. No. 19;
:ive 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91303098.7
FILLING DATE: 09-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00627
ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                     COMPUTER READABLE FORM:
BUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 317-276-3589
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.0
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D. C. COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                      USA
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US-08-129-129-6
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 4, 2002, 10:15:07 Run on:

; Search time 19.61 Seconds
(without alignments)
965.303 Million cell updates/sec

US-09-299-139A-1 Title: Perfect score:

1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283138 seqs, 96089334 residues Searched:

0 Word size : Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_71:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cript	tumor pecrosis fac	hetical pr			avermectin B 5-0-m	ltr	hypothetical prote	>		alpha-amylase (EC	0	nitrodenase molybd	_		adenylosuccinate s	probable 5'-nucleo		hypothetical prote			petH protein - Syn	hypothetical prote		н		~ન	probable atpE prot	cal p	Ď,
SUMMARIES		154182	13	m	CO.	JC6531	T44579	G86263	T07372	JT0946	JC7138	G82241	G69075	T18904	T35817	AI3295	A82447	S72635	A89959	S30855	S18766	D42194	D90762	E85625	T02924	H90913		E70774	E97642	AG2865
	DB	2	~	~	7	7	7	7	~	7	7	7	7	7	7	7	7	7	7	7	7	ď	7	~	7	7	7	7	~	7
	Length	435	107	189	265	283	283	328	391	437	437	449	459	474	504	520	580	14	1274	75	61	63	63	63	68	75	81	81	87	87
o¥	Query	100.0	3.6		3.6	٠		3.6	•		•		٠	3.6	٠	٠		٠		3.6		٠		٠	•		3.0		•	3.0
	Score	197	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	9	9	9	9	9	9	9	9	9	ø
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181 TTCKNPLEPLPPEMSGT 197 

RESULT H97132

hypothetical protein CAC1887 [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001 C; Accession: H97132 R; Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

30 6 3.0 89 2 C55587 31 6 3.0 89 2 C70847 32 6 3.0 93 2 S58674 33 6 3.0 107 2 S6399 34 6 3.0 107 2 T49916 35 6 3.0 110 1 S6399 36 3.0 111 2 C69946 37 6 3.0 111 2 C69946 38 6 3.0 112 2 H72689 39 6 3.0 112 2 H72689 41 6 3.0 112 2 A7252 44 6 3.0 124 2 G9598 45 6 3.0 124 2 G9598 46 3.0 124 2 G9598 47 10	1  1  1  1  1  1  1  1  1  1  1  1  1	89 2 C558 89 2 C758 89 2 C758 93 2 S588 107 2 S63 111 2 S63 111 2 C69 111 2 C69 111 2 H785 112 2 H785 112 2 T40 124 2 G95 124 2 C72 128 2 T40 128 2 T40 129 2 T40 129 2 T62 129 3 T62 129 3 T62 130 2 MID: 932 110 932 120 131 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	r c c c c c c c c c c c c c c c c c c c	GOMMENTS  GOMMENTS  GA-May-1996 # Lext_ch  24-May-1996 # Lext_ch  7.J.; Van den Berghe,  a hncDNA library of  81  GB/EMBL/DDBJ  7761; PIDN:AAA36757.1  7761; PIDN:AAA36757.1	acyl carrier prote probable whi82 pro RNA-binding protei thioredoxin trxA - thyorhettical prote thyothettical prote hypothettical prote sa ribosomal protein hypothettical expor hypothettical sa ribosomal prote 50S ribosomal prot human 12p transcribed seq human 12p transcribed seq eceptor repeat homology
Best Local Matches 19	<pre>1 Similarity 100 197; Conservative</pre>	100 vative	*	<pre>Pred. No. 1.2e-204; ; Mismatches 0; Indels</pre>	0; Gaps 0;
Qy 1 SQP(   1   1   Db 28 SQP(	QAVPPYASEN(              QAVPPYASEN(	QTCRDQ!          QTCRDQE	SKE)	SOPQAVPPYASENOTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 	AENS 60       AENS 87
Qy 61 YNE       Db 88 YNE	HWNYLTICQL(            HWNYLTICQL(	CRPCDP1 	ZWG1	YNEHWNYLTICOLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 	LLSD 120        LLSD 147

us-09-299-139a-1.rpr

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C.Superfamily: bloc homology
C.Keywords: methyltransferase
F;68-172/Domain: bloc homology <BIOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conserv
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                               169 LVEAAPG 175
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66 LVEAAPG 72
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T44579
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G86263
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                                  ŏ
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClA; Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97132
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-107 <KUR>
A;Reperimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene: CAC1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: C81134
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-189 < csto>
A; Cross-references: GB: AE004825; GB: AE004091; NID: 99950284; PIDN: AAG07473.1; GSPDB: GN001
A; Experimental source: strain PA01
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molybdate-binding protein homolog MopA - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: F36914
R;Wang, G;, Angermuller, S; Klipp, W.
B:Wang, G;, Angermuller, S; Klipp, W.
A;Title: Characterization of Rhodobacter capsulatus genes encoding a molybdenum transpor
A;Reference number: A36914; MUID:93259949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: C83134
R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable pilin PA4086 [imported] - Pseudomonas aeruginosa (strain PA01)
C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: F36914
A;Status: preliminary
A;Status: DNA
A;Moleoule type: DNA
A;Residues: 1-265 <WAN>
A;Note: sequence extracted from NCBI backbone (NCBIN:131915, NCBIP:131921)
C;Superfamily: molybdate-binding protein
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 18;
iive 0; Mismatches
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100.0%; Pred. No. 14;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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avermectin B 5-O-methyltransferase (EC 2.1.1..) - Streptomyces "avermitilis" C; Species: Streptomyces "avermitilis" C; Species: Streptomyces "avermitilis" C; Species: Streptomyces "avermitilis" C; Species: O5-Dec-1998 #sequence_revision O5-Dec-1998 #text_change 16-Jul-1999 C; Accession: JG6531 R; Ikada, H; Wang, L, R; Ohta, T; Inokoshi, J; Omura, S. Gene 206, 175-180, 1998 A; Title: Cloning of the gene encoding avermectin B 5-O-methyltransferase in avermectin A; Reference number: JG6531; MUID:98137789
                                                                                                                                                                                                                                                                                        A;Accession: JC6531
A;Molecule type: DNA
A;Residues: 1-283 <IKE>
A;Experimental source: wild type K139
C;Comment: This enzyme catalyzes the methylation of the hydroxyl group at the C5 pos1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyketide anthelminti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C5-0-methyltransferase [imported] - Streptomyces avermitilis
C;Species: Streptomyces avermitilis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C.Accession: T44579
R.Ikeda, H.; Nonomiya, T.; Usami, M.; Ohta, T.; Omura, S.
Proc. Natl. Acad. Sci. U.S.A. 96, 9509-9514, 1999
A;Title: Organization of the biosynthetic gene cluster for the parameter of the prospersion: T44579
A;Accession: T44579
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 283;
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100.0%; Pred. No. 20;
ive 0; Mismatches
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100.0%; Pred. No. 20;
Live 0; Mismatches
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A; Residues: 1.449 <HEL>
A; Cross-references: GB:AE004191; GB:AE003852; NID:99655568; PIDN:AAF94267.1; GSPDB:GN
A; Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase (EC 3.2.1.1) isozyme III - rice
NyAlternate names: 1.4-gulcan glucanohydrolase III
C;Species: Oryza sativa (rice)
C;Date: Oryza sativa (rice)
C;Date: 04-War-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7138; PC7040
C;Accession: JC7138; PC7040
C;Accession: JC7138; PC7040
C;Accession: JC7138; PC7040
A; A; Ayagai, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.
Biosci. Biotechnol. Biochem. 63, 1329-1335, 1999
A;Title: Characterization of chimeric enzymes constructed between two distinct alpha-A;Reference number: JC7137; MUID:99430781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 246-253 <a href="AB2">Aba2</a>
C;Comment: This enzyme Actalyzes the hydrolysis of internal alpha-glucosidic linkages
is important in germinating seeds and presenting as multiple isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: G82241
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers chardson, D.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein VC1108 [imported] – Vibrio cholerae (strain N16961 ser
                                                                                                               PIDN: AAA33896.1; PID:g169773 homology
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A;Map position: 1
C;Superfamily: Haemophilus influenzae conserved hypothetical protein HI1590
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Reywords: calcium binding; germination; glycosidase; hydrolase;
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                                               A;Molecule type: DNA
A;Residues: 1-437 <HUA>
A;Cross-references: GB:M59352; GB:M36985; NID:g169772;
C;Superfamily: wheat alpha-amylase; alpha-amylase core
F;171-315/Domain: alpha-amylase core homology <AMY>
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100.0%; Pred. No. 28;
ive 0; Mismatches
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Pred. No. 28;
0; Mismatches
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100.0%; Pre
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Best Local Similarity 100...
7; Conservative
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Matches 7; Conserv
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A; Residues: 1-437 <ABE>
A; Accession: PC7040
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               A;Status: preliminary
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90 GTEAELK 96
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Plant Physiol. 108, 1623-1629, 1995
Affitle: Witochondrial pyruvate dehydrogenase. Molecular cloning of the El alpha subunit A; Reference number: Z15993; MUID:95388769
A; Accession: T07372
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R; Huang, N.; Kolzumi, N.; Reinl, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A; Title: Structural organization and differential expression of rice alpha-amylase genes A; Reference number: JT0945; MUID:91088278
ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
Mature 408, 816-820, Mature 408, Marziali, M
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) El alpha chain - potato
C;Species: Solanum tuberosum (potato)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T07372
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
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A; Residues: 1.391 <GRO>
A; Torss.references: EMBL: Z26949; NID: g473168; PIDN: CAA81558.1; PID: g473169
A; Experimental source: cv. Desiree; tissue type leaf
C; Genetics:
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100.0%; Pred. No. 22;
iive 0; Mismatches
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Best Local Similarity 100.'
Matches 7; Conservative
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A; Molecule type: DNA
A; Residues: 1-328 <STO>
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C; Complex: heterot
C; Function:
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probable Glu-tRNA(Gln) amidotransferase chain B - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: OS-Nov-1999 #text_change 21-Jan-2000 C; Date: OS-Nov-1999 #text_change 21-Jan-2000 C; Date: OS-Nov-1999 #text_change 21-Jan-2000 R; Murphy, L; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1999 A; Reference number: 221589 A; Recession: T35817 A; Recession: T35817 A; Accession: T35817 A; Accession: T35817 A; Residues: DNA A; Residues: 1-504 ckurs A; Residues: 1-504 ckurs A; Residues: 1-504 ckurs A; Coebb: Scape Coebb: Scap
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100.0%; Pred. No. 32;
tive 0; Mismatches
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity 100.0
Matches 7; Conservative
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C;Superfamily: PET112 protein
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266 MGLEEIA 272
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18 DPVMGLE 24
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A; Map position: I
C; Keywords: ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrogenase molybdenum-iron protein, Nifk subunit - Methanobacterium thermoautotrophicum c; Species: Methanobacterision 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Jun-1999 C; Accession: G69075 R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S. Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514 A; Reference number: A690075 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Mesidues: 1-459 cMTH> A; Mesidues: 1-459 cMTH> A; Mesidues: 1-459 cMTH> A; Mesidues: 1-459 cMTH> A; Experimental source: strain Delta H
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A;Molecule type: DNA
A;Residues: 1-474 <WIL>
A;Coss-references: EMBL:269716; PIDN:CAA93527.1; GSPDB:GN00028; CESP:C04B4.2
A;Experimental source: clone C04B4
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18904
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                                      DB 2;
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                                      3.6%; Score 7; DB 2
100.0%; Pred. No. 29;
Live 0; Mismatches
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A;Gene: MTH1564
C;Superfamily: dinitrogenase beta chain
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A;Gene: CESP:CO4B4.2
A;Map position: X
A;Introns: 67/3; 161/2; 207/3; 435/1
Query Match
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7; Conservative
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decides Brucella melitensis (EC 6.3.4.4) [imported] - Brucella melitensis (strain 16M C;Species: Brucella melitensis (C.3.4.4) [imported] - Brucella melitensis (Strain 16M C;Species: Brucella melitensis (C.3.4.4) [imported] - Brucella melitensis (Species: Ol-Feb-2002 #sequence_revision Ol-Feb-2002 #text_change Ol-Feb-2002 (C.3.4.2.4) [imported] Mazur, M.3.5 (Mazur, M.3.5) [imported] Mazur, M.3.6 (Mazur, M.3.6) [imported] Mazur, M.3.6 (Mazur, M
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100.0%; Pred. No. 33;
tive 0; Mismatches
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2002, 10:16:57; Search time 11.95 Seconds

(without alignments)
638.306 Million cell updates/sec

Title: US-09-299-139A-1
Sequence: 197
Scoring table: 180PQAVPPYASENGTCRDGE......QSDTTCRNPLEPLPPEMSGT 197
Scoring table: OLIGO
Gapop 60.0, Gapext 60.0
Searched: 105224 seqs, 38719550 residues
Word size: 0
Total number of hits satisfying chosen parameters: 105224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Listing first 45 summaries

SwissProt\_40:\*

Database :

## SUMMARIES

	Description	941 homo sapien	mus m	P58081 streptococc		~	P52004 brucella ab	_	027606 methanobact	P95296 methanobact	Q9z578 streptomyce		P32634 saccharomyc	P31358 homo sapien		P45828 mycobacteri	Q10598 mycobacteri	-	P21609 clostridium	-	P45939 bacillus su	051351 borrelia bu		414 guillardia		352 brassica na		_			_		O	412 cuphea lanc
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SUMMARIES	ID	TNR3_HUMAN	TNR3_MOUSE			SOLTU	PURA_BRUAB	AM3E_ORYSA	NIFK_METTH	NIFK_METTM	GATB_STRCO	WEE1_RAT	YEW2_YEAST	CD52_HUMAN	YPH2_SYNP2	ATPL_MYCLE											ACP2_BRANA		ACP5_BRANA	ACP_BRACM	YHCB_HAEIN	CASGL	ARATH	ACP2_CUPLA
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1 ACP4_CUPLA 1 ACP1_CUPLA 1 NIU2_RHOCA 1 ACP3_CUPLA 1 PP1B_BACSU 1 ACP1_HORVU 1 NDK1_ORYSA 1 NDK2_ARCFU 1 ACP2_ARCFU 1 ACP2_ARCFU 1 RAO5_ORYSA 1 RSVR_COTJA	ALIGNMENTS	HUMBAN  PRES, HUMAN  PRES, HUMA	LLO H X O
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44 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		TUR3_HUMAN  TUR3_HUMAN  TUR3_HUMAN  TUR3_HUMAN  TUR3_HUMAN  TUR3_HUMAN  TUR3_HUMAN  TUR5_1: 29, Last sequen  T16_CT_2001 (Rel. 29, Last sequen  E2 related protein) (Tumor necrosi  LTBR OR TWFCR OR TWFRSF3.  SO HOMO saplens (Human).  C EURATYOLE MELAZOA: Chordata; Cra  MAMMALIA EURATOA: MetaZoa; Chordata; Cra  MANDLINE-9325381; Pubmed-8486360;  RN [1]  RR SEQUENCE FROM N.A.  RCONSTRUCTION N.A.  RY MEDLINE-93252381; Pubmed-8486360;  RR ABDELINE-94225209; Pubmed-8171323;  RY MEDLINE-94225209; Pubmed-8171323;  RY MEDLINE-94225209; Pubmed-8171323;  RY MEDLINE-94225209; Pubmed-8171323;  RY MEDLINE-94225209; Pubmed-8171323;  CCOMPANDE SECEPTOR FOR THE LY  TANDROMEN BEVELOPMENT.  CC TIMMUND BEVELOPMENT.  CC TIMMUND BEVELOPMENT.  CC TIMMUND BEVELOPMENT.  CC THIS SMISS-PROT entry is copyrigh  Detween the Swiss Institute of B  CC THIS SMISS-PROT entry is copyrigh  Detween the Swiss Institute of B  CC TS end an enail to licensee agree  CC TS EMBL; LO4270; AAA36757.1; .  DR RSSP PESS2 INFR_C6; 4.  DR PTAMP, SO00209; TWFR_C6; 1.  DR PRODON; TWFR_C6; 1.	Receptor; Tre SIGNAL CHAIN DOMAIN
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-i - SUBCELLULAR LOCATION: Type I membrane protein.
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TWER-CYS 2.
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BY SIMILARITY
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SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / Serotype M1;
MEDLINE-21192684; PubMed-11296296;
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MGD; MGI:104875; Ltbr.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
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Best Local Similarity 100.
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179
415 AA;
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-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                  61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
                                                                                                                                                                                                                                                                                            88 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAWALECTHCELLSD 147
                                                                                                                                                                                                                                                                                                                         121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                          SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
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624626E6022F656F CRC64;
  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                   100.0%; Score 197; DB 1; i 100.0%; Pred. No. 8.3e-202; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                         SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     415 AA
                                                  SIMILARITY
                                                                       SIMILARITY
                                                                                SIMILARITY
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                                                                                                                                           SIMILARITY
          TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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01-0CT-1996 (Rel. 34, Last sequence
16-0CT-2001 (Rel. 40, Last annotatio
Lymphotoxin-beta receptor precursor.
LTBR OR TNFCR OR TNFRSF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                   BY
BY
BY
BY
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BY
BY
BY
                                                                                                                                                                        46709 MW;
                                                                                                                                                                                                                                                                                                                                                                 181 TTCKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
 435
811
24
1168
211
58
72
80
80
80
116
117
1132
1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                        135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
 TNR3_MOUSE
P50284;
                                                                                         DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Honjo T.;
                                                  DISULFID
DISULFID
DISULFID
                                                                                                                               DISULFID
                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                               DISULFID
                                                                                                                                                                        SEQUENCE
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
TNR3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYMPHOTOXIN-BETA RECEPTOR. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Transmembrane; GlyCoprotein; Repeat; Signal.
1 30 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINKED (GLCNAC. . .) (P
29B326A566AEF661 CRC64;
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RAPARA RA

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
ODPA_SOLTU
                                                                                                                                                                                                                                                                                                                                              Matches
               DR DR DR ETT SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                          POGNETA: " CONTROL SCI. U.S.A. 98:4658-4663(2001).
PYOGENES.";
PROC. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
-!- FONCTION: IF-3 BINDS TO THE 30S RABDSOMAL SUBUNIT AND SHIFTS THE EQUILIBRUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olan Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 33303 / B10;
MEDLINE-93259949; Pubmed-8491722;
Wang G., Angermueller S., Klipp W.;
Wang cterization of Rhodobacter capsulatus genes encoding a
molybdenum transport system and putative molybdenum-pterin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initiation factor; Protein blosynthesis; Complete proteome.
SEQUENCE 176 AA; 20053 MW; FD3247FB6C9D5919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 176;
                                                                                                                                                                                                                                                                                                           SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION
--- SUBUNIT: MONOMER (BY SIMILARITY).
--- SUBCELLULAR LOCATION: CYLOPIASMIC.
--- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0KR-2002 (Rel. 41, Last annotation update)
.Molybdenum-pterin binding protein mopA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 7; DB 1
100.0%; Pred. No. 5.6
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 175:3031-3042(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006531; AAK33741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001288; IF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002880; IF3; 1. PROSITE; PS00938; IF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00707; IF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1061;
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53 QPQAVPP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QPQAVPP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOPA_RHOCA Q08385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Millar A.H., Knorpp C., Leaver C.J., Hill S.A.;
"Plant mitochondrial pyruvate dehydrogenase complex: purification and identification of catalytic components in potato.";
Biochem. J. 334:571-576(1998).
-!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pyruvate dehydrogenase El component alpha subunit, mitochondrial precursor (EC 1.24.1) (PDHE1-A).
Solanum tuberosum (Potato).
Enkaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NOBL_TAXID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grof C.P., Winning B.M., Scaysbrook T.P., Hill S.A., Leaver C.J.; "Mitochondrial pyruvate dehydrogenase. Molecular cloning of the El alpha subunit and expression analysis."; Plant Physiol. 108:1623-1629(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyldihydrolipoamide + CO(2).
--- COFACTOR: THIAMINE PYROPHOSPHATE.
--- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA
                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT (BY SIMILARITY).
-!- SUBUNIT TETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                 Length 265;
                                                                                                                                                                                                                        Indels
                                                                                                                       7EB89FC938CAF326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S
                                                                                                                                                                                 DB 1;
. 8;
                                                                                                                                                                               Score 7; DB 1; Pred. No. 8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                  MOP-LIKE.
                                                                                                       MOP-LIKE
                                                                                                                                                                 3.6%; SCUL.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. DESIREE; TISSUE-Leaf;
MEDLINE-95388769; PubMed-7659754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. ROMANO; TISSUE-Tuber;
MEDLINE-98399821; PubMed-9729464;
EMBL, L06254; AAA71912.1; -.
InterPro; IPR003725; ModE.
Pfam; PF02573; ModE; 1.
Transport; Molybdenum; Repeat.
REPEAT 125 MOF
REPEAT 193 265 MOF
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
                                                                                                                       265 AA; 27119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z26949; CAA81558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001017; El_dh.
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 27-42.
                                                                                                                                                                                                                                                              169 LVEAAPG 175
                                                                                                                                                                                                                                                                                                   66 LVEAAPG 72
                                                                                                                                                                                                                                                                                                                                                                                                    ODPA_SOLTU
P52903;
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12;

Pred. No.

100.08;

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Best Local Similarity
                                                                                                                AM3E_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
CA_BIND
CA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                     AM3E_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
            Matches
                                    δ
                                                        g
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished observations (NOV-1999).
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE NUCLEOTIDE BIOSYNTHESIS.
-!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
Pfam; PF00676; El_dehydrog; 1.
glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate; Phosphorylation; Mitochondrion; Transit peptide.
TRANSIT MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XKYVRHIEEL -> SNMSAISKS (IN REF. 1).
                                             PYRUVATE DEHYDROGENASE E1 COMPONENT
                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                           ;
0
                                                                                                     Length 391;
                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Tatum F.M., Steckelberg M.A.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                         ALPHA SUBUNIT.
F9110B374B022F0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F443CFAE8D10EE75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF A PROBABLE C-TERMINAL FRAMESHIFT.
                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSY; TAZZO: INDEX.

PÉTAZZO: INDEX.

PÉTAZZO: INDEX.

PÉTAZZO: PRODILIS: Adenylsucc_synt.

PRODIN: PRO0709; Adenylsucc_synt; 1.

PRODIN: PRO01188; Adenylsucc_synt; 2.

PROSITE: PS00513; ADENYLOSUCCIN_SYN_2; 1.

PUTINE biosynthesis; Ligase; GTP-binding.

NP_BIND 12 18 GTP (POTEWILL).
                                                                                                                                                                                                                              402 AA
                                                                                                   3.6%; Score 7; DB 1
100.0%; Pred. No. 11;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last seq
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43919 MW;
                                                                    43228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L43054; AAA75455.1; -.
HSSP; P12283; 1ADE.
                                                                                                                                                                                                                                                                                                 (ADSS) (AMPSase) (Fragment)
                                                                                                                           Conservative
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                             Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenylosuccinate.
                                                                    391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 AA;
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                 125 TEAELKD 131
                                                                                                                                                                      332 TEAELKD 338
                                                                                                                                                                                                                                                                                                                      Brucella abortus
                                      27
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=2308;
                                                                                                                                                                                                                            FURA_BRUAB
P52004;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Michoud K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE CONFLICT
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                        9
                                                                                                                                                                                                                   PURA_BRUAB
                                                                                                                           Matches
  DR
KW
FT
FT
SQ
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                                                                                                                                                                      Q
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DB 1; Length 402;

3.6%; Score 7;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
    Gaps
                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-amylase isozyme 3E precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-EV. JAPONICA M202; TISSUE-Etiolated leaf;
MEDLINE-91088278; PubMed-2263460;
MEDLINE-910807N; Noizumi N., Realil S., Rodriguez R.L.;
"Structural organization and differential expression of rice alpha-
                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000461; Alpha_amylase.
Pam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amylase genes.";
Nucleic Acids Res. 18:7007-7014(1990).
-!- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 437;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-AMYLASE ISOZYME 3E.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A; COE8276CCEA16602 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%; Score 7; DB 1;
100.0%; Pred. No. 12;
iive 0; Mismatches
                                                                                                                                                                                                         437 AA.
    Mismatches
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01-AUG-1992 (Rel. 23, Last seq
15-DEC-1998 (Rel. 37, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; JT0946; JT0946.
HSSP; P04063; lAVA.
Mendel; 9691; ORYsa;Amyl;4.
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    Conservative
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                                                                                                                                                                                                             STANDARD;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                 glucanohydrolase).
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116
175
437 #
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175 MGLEEIA 181
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                                               81 MGLEEIA 87
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RESULT 8 NIFK\_METTH

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459 AA.
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     STANDARD;
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                                                                                                                                                                         Methanothermobacter.
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=79929;
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GATB OR SC8D9.13.
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   NIFK_METTM
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GATB_STRCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Partison D., Hoang L., Reagle P., Lumm W., Pothier B., Giu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Silmer G., Goyal A., Pietrovski S., Church G., Goyal A., Pieterovski S., Church G., Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00148; oxidored_nitro; 1.
PROSITE; PS00090; NITROGENASE_1_2; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 7; DB 1; Length 459;
100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 AA; 51489 MW; F2CB731BCC675AC9 CRC64;
                                                                                                                     459 AA.
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                                                                                                                                                                                                                   (Nitrogenase component I) (Dinitrogenase).
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InterPro; IPR000510; Oxidored_nitrognse_1.
                                                                                                                                                                                                                                                      Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                         STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000916; AAB86038.1; -.
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                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                    Methanothermobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 459 AA;
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID=145262;
124 GTEAELK 130
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EYYEPQH 454
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90 GTEAELK 96
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                                                                                                                    NIFK_METTH
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-) (Glu-ADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID=1902;
                                                                                                                                                           Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133)
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Nitrogenase molypdenum-iron protein beta chain (EC 1.18.6.1)
(Nitrogenase component I) (Dinitrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00148; oxidored_nitro; 1.
PROSITE; PS00090; NITROGENASE_1_2; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
SEQUENCE 459 As; 51158 MW; 04F03EA9CB3E9E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 459;
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                                                                                                                                                                                                                                                                                                                 Hochheimer A.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No. 13;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxidored_nitrognse_1.
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Query Match

Best Loc Matches

448

δ g RESULT

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**LEURODU A.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.

**LEURODU A.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.

**C-I-PUNCTION: MAY ACT AS A BEGATIVE REGULATOR OF ENTRY INTO MITOSIS

**C-I-PUNCTION: MAY ACT AS A BEGATIVE REGULATOR OF ENTRY

**C-I-CATALYTION: BY PROTECTING THE NUCLEUS FROM

**C-I-CATALYTION: BY PROTECTING THE NUCLEUS FROM

**C-I-CATALYTION: BY PROTECTION THE NUCLEUS SAND G2 PHASES

**ACTIVITY INCREASED DUECA BEFORE THE

**C-I-CATALYTION: SPECIFICALLY PHOSPHORYLATES AND

**C-I-CATALYTION: SPECIFICALLY PHOSPHORYLATES AND

**C-I-CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by an on-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
tyrosine phosphate. BYANTHESIS IS INCREASED DURING S AND G2 PHASES, PRESUMABLY BY AN INCREASE IN TRANSCRIPTION; ACTIVITY IS DECREASED BY PHOSPHORYLATION DURING M PHASE. PROTEIN LEVELS FALL IN M PHASE AS A RESULT OF DECREASED SYNTHESIS COMBINED WITH DEGRADATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                               7B05B23268146CDA CRC64;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           063802;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Weel-like protein kinase (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  646 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; L
Pred. No.
                                                                                                                                                                                                                                                                            EMBL; AL035569; CAB37577.1; -.
InterPro: IPR0007389; DUF186.
InterPro: IPR00173; Gln_amidotransf_B.
Pfam; PF02637; DUF186; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%; Scor
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                               504 AA; 54485 MW;
                                                                                                                                                                                                                                                                                                                                                                                 Protein biosynthesis; Ligase.
                                                                                                                                                                                                                                                                                                                                    Pfam; PF01162; GatB; 1.
Pfam; PF02934; GatB_N; 1.
PROSITE; PS01234; GATB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
               ENTRY INTO MITOSIS, ALTHOUGH N-TERMINAL PHOSPHORYLATION MIGHT ALSO REGULARE THE PROTEIN STABILITY VIA PROTECTION FROM PROTEOLYSIS OR MIGHT REGULATE THE SUBCELLULAR LOCATION (BY SIMILARITY)
SUBUNIT: BINDS TO 14-3-3 PROTEIN ZETA.
ACTIVITY SEEMS TO BE NEGATIVELY REGULATED BY PHOSPHORYLATION UPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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STRAIN=S288C / AB972;
Dietrich E.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Adviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY CDC2) (POTENTIAL). PHOSPHORYLATION (BY CDC2) (POTENTIAL). 740120F51C811DAF CRC64;
                                                                                -:- SUBCELLULAR LOCATION: Nuclear (By similarity).
-:- PTM: PHOSPHORYLARED DUBRING M AND GI PHASES. ALSO
-- ATTOPHOSPHORYLARED (By similarity).
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-CCT-1993 (Rel. 27, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 195.4 kDa protein in RPS26B-GLC7 intergenic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ်
                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00107; PROTEIN KINASE_ATP: 1.
PROSITE: PS00107; PROTEIN KINASE_ATP: 1.
PROSITE: PS00108; PROTEIN KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN KINASE_DOM; 1.
Mitosis: Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Копр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., F
Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 7; DB 1
100.0%; Pred. No. 18;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY - ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLU
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam: PR00069: pkinase: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Nuclear protein. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                        EMBL; D31838; BAA06624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
568
312
327
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123
139
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                                                                                                                                                 WEEL SUBFAMILY.
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298
304
327
425
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P32634;
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SEQUENCE
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Best Local Similarity
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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-!- FUNCTION: MAY PLAY A ROLE IN CARRYING AND ORIENTING CARBOHYDRATE, AS WELL AS HAVING A MORE SPECIFIC ROLE.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- DATABASE: NAME-PROW: NOTE-CD guide CD52 entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd52.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-53119668; pubMed=8418821;
Kirchhoff C., Krull N., Pera I., Ivell R.;
"A major mRNA of the human epididymal principal cells, HE5, encodes
the leucocyte differentiation CDw52 antigen peptide backbone.";
Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xia M.-Q., Tone M., Packman L., Hale G., Waldmann H.; "Characterization of the CAMPATH-1 (CDw52) antigen: biochemical analysis and cDNA cloning reveal an unusually small peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
CAMPATH-1 antigen precursor (CD52 antigen) (CDW52) (Cambridge pathology I antigen) (Epididymal secretory protein E5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein.
1753 AA; 195382 MW; E4252998C6C2508B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.6%; Score 7; DB 1;
100.0%; Pred. No. 42;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 21:1677-1684(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Spleen;
MEDLINE=91285018; PubMed=1711975;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; U18916; AAC03230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              PIR; S30855; S30855.
SGD; S0000934; PMD1.
InterPro; IPR001799; Kelch.
Pfam; PF01344; Kelch; 2.
Hypothetical protein.
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Epididymis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
CD52_HUMAN
ID CD52_HUMAN
AC P31358;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-92207922; PubMed=1554697; Schluchter WM., Bryant D.A.; Schluchter WM., Bryant D.A.; Molecular characterization of ferredoxin-NADF+ oxidoreductase in cyanobacteria: cloning and sequence of the petH gene of Synechococus sp. PCC 7002 and studies on the gene product."; Blochemistry 31:3092-3102(1992). - - - SIMILARITY: CONTAINS I RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                         Antigen; Signal; Glycoprotein; GPI-anchor; Membrane; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
Hypothetical protein in petH 3'region (Fragment).
Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
Bacteria: Cyanobacteria: Chroococcales: Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                   REMOVED IN MATURE FORM (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_005130.
4AE2A056682BEEA6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                            CAMPATH-1 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.0%; Score 6; DB 1
100.0%; Pred. No. 25;
rative 0; Mismatches
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Pred. No.
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                                                                                                                                                          EMBL; X62466; CAA44323.1; -. EMBL; X67699; CAA47929.1; -. EMBL; A23013; CAA01644.1; -. PIR; S18766; S18766. MIM; 114280; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6614 MW;
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KESULT 14
YPH2_SYNP2
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Mungall K., Basham D., Brown D., Chillingworth T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
A. Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
A. Murphy L., Oliver K., Simon S., Simmonds M., Skelton J., Squares R.,
A. Rutter S., Seger K., Simon S., Simmonds M., Skelton J., Squares R.,
A. Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
A. Barrell B.G.;
Mature 409:1007-1011/2001).
C. FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC
COMPONENT (FCF) SUBBUILT) OF THE ATPASE COMPLEY.
COMPONENT (FCF) SUBBUILT) OF THE ATPASE COMPLEY.
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CHANTIES ALEHAR(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
CHAIN FAMILY: BELONGS TO THE ATPASE CHAIN FAMILY.
C. ISHMILARITY: BELONGS TO THE ATPASE CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DICYCLOHEXYLCARBODIIMIDE (BY SIMILARITY).
E5456207EE9E0C13 CRC64;
    Gaps
                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterlum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding;
                                                                                                                                                                                      ou-NOV-1995 (Rel. 32, Created)
16-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP synthase C chain (EC 3 6.3.14) (Lipid-binding protein)
(Dicyclohexylcarbodiimide-binding protein)
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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  Mismatches
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MEDLINE-21128732; PubMed=11234002;
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InterPro: IPR000454; ATPase_C_eub.
Pfam; PF00137; ATP-synt_C; 1.
PROSITE; PS00605; ATPASE_C; 1.
  0
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  Conservative
                                                                                                                                                                              STANDARD;
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P45828;
01-NOV-1995 (Rel.
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                                      80 VMGLEE 85
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Ouery Match
Best Local Similarity 3.04; Score 6, DB 1; Lenyth 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 168 GIVPA 173
Db 58 GIVPA 63
Search completed: October 4, 2002, 10:20:49
Job time: 232 sec
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OM protein

Run on:

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096031 homo sapien
Q9h5c7 homo sapien
Q924i0 mus musculu
Q921d6 mus musculu
                                                                                                                                                                                                                                                                                    093hj3 streptomyce
09uvn5 alternaria
09uch8 homo sapien
09f0n6 bacillus am
09bw46 homo sapien
                                                                                                                                         O9dc40 mus musculu
O91vq3 mus musculu
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09c093 homo sapien
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O9de14 xenopus lae
                                 0941s5 oryza sativ
09km44 vibrio chol
                                                                                                                                                                                                                Q9r095 rattus norv
                                                        09h5q7 homo sapien
09ui92 homo sapien
096031 homo sapien
            091211 streptomyce
09rkx6 streptomyce
                                                                                                                                                                 Q60045 thermoanaer
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017620 caenorhabdi
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Q9nkt1 leishmania
                                                                                                                                  Q9vta3 drosophila
                                                                                                                                                                                                                             Q9nku5 leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
Meelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng O.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium. NCBL_TaxID=1488;
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EMBL; AE007697; AAK79851.11; -

Hypothetical protein; Complete proteome.

SEQUENCE 107 AA; 12489 MW; 3DE26914B72DF0F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN CAC1887.
                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AA
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Q9DC40
Q91VQ3
Q60045
Q99TC3
Q9C093
Q9C093
                      Q9RKX6
Q941S5
Q9KM44
Q9H5Q7
Q9U192
Q96031
Q9H5C7
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Q9Q8G7
Q9Z5F4
Q9NKT1
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Q921D6
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Best Local Similarity
Matches 7; Conserv
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Q92rw6 rhizobium m
Q97ce9 thermoplasm
Q9ksz8 vibrio chol
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Q12953 homo sapien
Q9djrl citrus tris
Q9frll lycopersico
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1282.650 Million cell updates/sec
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09h611 homo sapien
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Q9pus0 salvelinus
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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us-09-299-139a-1.rspt

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STRAIN=JCM 10545 / 7;

PubMed=11572479;

Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Cshima T., Kikuchi H.,
"Complete genome sequence of an aerobic thermoacidophilic
Cirenarchaeon, Sulfolobus tokodaii strain?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STROINE—2043737; Pubmed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Shencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                         Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus
NCBI_TaxID=111955;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                               DNA Res. 8:123-140(2001).

EMBL, AP000989; BAB67255.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 150 AA; 17433 MW; 5262C811B145D43B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 AA; 19718 MW; B76DED0410BD4308 CRC64;
                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN
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Last annotation update)
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                 150 AA.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
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                 PRELIMINARY;
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                                                                                                                      Sulfolobus tokodaii.
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Best Local Similarity
Matches 7; Conserv
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PA4086.
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL596030; CAC44282.1;
Hypothetical protein.
SEQUENCE 204 AA; 21680 MW; DC2C849468F88AA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tashiro H., Ota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%; Score 7; DB 2; Length 204; 100.0%; Pred. No. 34; 0; Indels live 0; Mismatches 0; Indels
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TISSUE-SMALL INTEGTINE;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO26545; BAB15456.1;
SEQUENCE 266 AA; 28907 MW; 0A291FB7E1339D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Neil S., Harris D.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 21.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22692 FIS, CLONE HSI11184.
                                                                                                                   204 AA
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                                                                                                                   PRT;
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                            SCBAC17F8.10C.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-A3(2);
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142 GLVEAAP 148
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Gaps

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0; Indels

Pred. No. 32, Mismatches

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Conservative

100.08;

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Gaps

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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pelle R.;
"Molecular cloning and characterization of Trypanosoma (Duttonella)
vivax inosine-adenosine-guanosine preferring (IAG-) nucleoside
                                                                                                                                                                                       ö
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0
                                                                                                                                                          Length 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrolase homolog.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF311(701. AAG38561.2;
InterPro; IPR001910; IUNH.
Pfam; PF01156; IU_nuc_hydro; 1.
Probom; PD007736; IUNH; 1.
                                                                                                                 302 AA; 34037 MW; E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 AA; 36330 MW; 034F9833FF6C2825 CRC64;
                                                                                                                                                                                                                                                                                                                                 09GPQ4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1AG-NUCLEOSIDE HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F3F19.1 PROTEIN.
                                                                                                                                                        3.6%; Score 7; DB 13;
100:0%; Pred. No. 47;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 7; DB 5
100.0%; Pred. No. 50;
tive 0; Mismatches
       PEGETS, TENGENCE, 4.
ProDom; PE00020; TNFR, 6; 1.
SMART; SMO2008; TNFR; 4.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR, NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 CTHCELL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 CTHCELL 251
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                                                                                                                                                                                                                                 1111111
38 RCPPGTY 44
                                                                                                                 SEQUENCE
                                                                                                  Receptor
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Q9SAD4;
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=99380548; PubMed=10449723;
Ikeda H., Nonomiya T., Usani M., Omura S.;
Ikeda H., Nonomiya T., Usani M., Omura S.;

"Organization of the biosynthetic gene cluster for the polyketide anthelmintic macrolide avermectin in Streptomyces avermitilis.";

Proc. Natl. Acad. Sci. U.S.A. 96:9509-9514(1999).

InterPro: IPR001601: Meth-transf.

InterPro: IPR001601: SAM_bind.

InterPro: IPR004033; ubiE_coofs_methyltransf.

Pfam: PF01209; Ubie_methyltran;

Transferase; Methyltransferase.
                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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Salvelinus fontinalis (Brook trout) (Brook char).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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                           Length 266;
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                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0676E02AD80BC094 CRC64;
                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 7; DB 2;
100.0%; Pred. No. 45;
iive 0; Mismatches
                                                                                                                                                                                    283 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 AA.
                        3.6%; Score 7; DB 4
100.0%; Pred. No. 42;
Live 0; Mismatches
                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e; Methyltransferase.
283 AA; 30113 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Reprod. 62:420-426(2000).
EMBL; AF156738; AAD56428.1; -.
HSSP; O14763; 1D4V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                             (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 18,
                                                      7; Conservative
                                                                                                                                                                                                                                                                                      Streptomyces avermitilis.
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                                                                                                                                                                                                                                                         C5-O-METHYLTRANSFERASE
                        Query Match
Best Local Similarity
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=33903;
                                                                                                              104 LLSDCPP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * 106 AAWALEC 112
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                                                                                117 LLSDCPP 123
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01-OCT-2001
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Q9SON6
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Gaps

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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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Best Local Similarity 100.
                                                                                                                                                                                         Query Match 3.6
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                              37
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                             SEQUENCE FROM N.A
                       NCBI_TaxID=12162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 TEAELKD 338
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| 128 YEPOHRI 134
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            osterovirus.
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NON_TER
SEQUENCE
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Q52181;
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Q9FR11
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Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A., Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M., Ecker J.R., Federspiel N.A., Theologis A.; Arabidopsis thaliana chromosome 1 BAC F3F19 sequence.", Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gmerek R.E., Medford J.I.;

"The complete sequence of a human hippocampus gene (HHCMA56) shows
homology to developmental genes from Arabidopsis and Brassica napus.";
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

EMBL; U13395; AAA21465.1;
SEQUENCE 370 AA; 41521 MW; BZFIC523F3ABAEFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                    DB 10; Length 328; . 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                          Submitted (Mar-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007357; AAD31052.1; -.
HSSP; 080337; 2GCC.
InterPro; IRRO01471; AP2-domain.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELENNT.
ProDom: P0001423; AP2-domain; 1.
SMART; SM00380; AP2, 1.
SEQUENCE 328 AA; 36319 MW; 66320534B5FCAE6B CRC64;
                                                                                                                                                                                                                                                            Indels
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Last annotation update)
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Last annotation update)
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. 56;
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                                                                                                                                                                                                                                      3.6%; Score 7; DB 1
100.0%; Pred. No. 50;
tive 0; Mismatches
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100.0%; Pred. No. 56;
tive 0; Mismatches
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Q12953;
Q1-090-1996 (TrEMBLrel. 01, Cr
Q1-NOV-1996 (TrEMBLrel. 01, La
Q1-DEC-2001 (TrEMBLrel. 19, La
OXIDOREDUCTASE.
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(TrEMBLrel. 16, I
(TrEMBLrel. 17, I
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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Q9DJR1;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
POLYPROTEIN (FRAGMENT).
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Theologis A.;
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Citrus tristeza virus.
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Q9DJR1
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
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Loe H.S., Kim I.J., Chung W.I.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF209924; AAG43499.1;
InterPro; IPR001017; El_dh.
Pfan; PF00676; El_dehydrog; 1.
NON_TER 1
SEQUENCE 391 AA; 43373 MW; 4ECDBF97E9DD7F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                3.6%; Score 7; DB 12; Length 371; 100.0%; Pred. No. 56; tive 0; Mismatches 0; Indels
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STRAIN=PB75;
Connor R.K., Hailstones D.L., Barkley P., Zhou C.;
Connor R.K. Hailstones D.L., Barkley P., Zhou C.;
Characterisation of Australian strains of CTV.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A3399541; CAC19973.1; -
InterPro; IPR000606; Viral, helicasel.
Pfam; PF01443; Viral_helicasel; 1.
                                                                                                                                                                                                                                                                    371 AA; 41728 MW; 0B6861589E74684A CRC64;
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Plasmid pCB2.4.
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCB1_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PYRUVATE DEHYDROGENASE (FRAGMENT).
Lycopersicon esculentum (Tomato).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 59;
iive 0; Mismatches
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KN Complete proteons
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                                                               "The complete DNA sequence and replication analysis of the plasmid pCB2.4 from the cyanobacterium Synechocystis PCC 6803."; Plasmid 31:131-137(1994).
EMBL: L25424; AAAA97418.1; -.
INTERFIC: IPRO3015; HHL Myc.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE FAD-DEPENDENT OXIDOREDUCTASE PROTEIN.
SMC00779.
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobiaceae; Sinorhizobium.
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100.0%; Pred. No. 61;
lve 0; Mismatches 0; Indels
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(TrEMBLrel. 18, Last sequence update)
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0; Mismatches
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                        STRAIN-PCC 6803;
MEDLINE-94302133; PubMed-8029321;
Yang X., McFadden B.A.;
"The complete DNA sequence and report of from the cyanobacterium Sy
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100.0%; Pre
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Best Local Similarity 7; Conservat
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SEQUENCE FROM N.A.
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238 EAELKDE 244
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26 PGTEAEL 32
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Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
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                                                                         Thermoplasma volcanium.
Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000)
EMBL; AP000991; BAB59294.1; -.
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100.0%; Pred. No. 64;
ative 0; Mismatches
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InterPro; IPR002293; AA_rel_permease_1.
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed_11121031;
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Best Local Similarity luv...
7; Conservative
                     TVG0161955 PROTEIN.
TVG0161955.
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Amino acid sequenc Wild type N-termna Human 40 kDa TNF i Human type 2 tumou

Tumour necrosis in

40kD TNF inhibitor Human TNF-R deduce Fibroblast derived Human tumour necro A human tumour nec Death receptor. H Human tumour necro Human 40 kDa TNF i Fusion protein TNF

STNFR(075):FC fusion pro Amino acid sequenc A K108F/K120R muta BamTP delta53 nerv Pig costimulatory Rodent protein seq

pro

TNF-R deduced from Tumour necrosis fa Protease-resistant Protease-resistant

Rat INFR (p80) TNFR:Fc fusion

Human type 2 tumou (p80) ext Peptide fragment o

Amino acid sequenc Human mFLINT #2 pr

FAS ligand

Human FLINT

Benjamin CD, Browning JL, Hochman PS;

(BIOJ ) BIOGEN INC.

WPI; 1997-132373/12

Tnfr2 protein. Un Human soluble tumo Tumour necrosis fa

11133 456 456 315 309 305 305

10 10 10 110

Score

No.

Result

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Human; lymphotoxin beta; receptor; blocking agent; extracellular; ligand binding; domain; treatment; Th1 cell; immune response; delayed; hypersensitivity; contact; tuberculin; granulomatous; graff versus host; disease, organ rejection; autoimune; disorder; multiple sclerosis; insulin dependent diabetes; uveitis; cytckine; sympathetic ophthalmia; psoriasis; Listeria; Toxoplasma; infection; Mycobacterium; abnormal; lymphoid organ; development.
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AAY95322
AAY77462
AAY94720
AAB50082
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AAY54443
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 21-JUL-1995;
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1 SQPQAVPPYASENQTCRDQE......QSDTTCKNPLEPLPPEMSGT 197
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                                                                                  The present sequence, a human lymphotoxin beta receptor (LT-beta-R) blocking agent, comprises the extracellular ligand binding domain blocking agent, comprises the extracellular ligand binding domain to fit the human LT-beta-R up to the transmembrane region. It can be used to treat a Thl cell mediated immune response which contributes to a delayed type hypersensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity graft versus host disease, organ rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin dependent diabetes, sympathetic conditions exacerbated by the activities of Th-1 type cytokines, or listeria, Toxoplasma or Mycobacterium infection. Its ability to selectively or partially block the LT-beta-R pathway may be useful in the treatment of abnormal lymphoid organ development associated with misexpression or overexpression of signalling by the LT-beta-R pathway. The present LT-beta-R blocking agent is capable of selectively inhibiting Thl, but not Th2 cell dependent immune effector mechanisms. As Thl cytokines can inhibit Th2 cell dependent responses, the present LT-beta-R blocking agent may also indirectly stimulate certain Th2 cell dependent responses which are normally inhibited by Th1 induced cytokines. Doses of about 1 mg/Kg of the present soluble LT-beta-R are expected to be suitable starting doses for optimising treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ta; LT-beta; LT-beta receptor; follicular dendritic cell; tumour; follicular lymphoma; extracellular domain; human.
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Compositions comprising lymphotoxin-beta receptor blocking agent used to treat auto:immune diseases, e.g. sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1133; DB 18; Length 197; Best Local Similarity 100.0%; Pred. No. 6.7e-84; Matches 197; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphotoxin (LT)beta-receptor extracellular region.
                                                          Example 1; Pages 55-56; 76pp; English.
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                               insulin-dependent diabetes, etc.
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The invention provides a method for arresting or reducing, severity of effects of a tumour by administration of a composition which inhibits the interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor of the interaction between LT-beta and its receptor can be administered for altering the survival or maintenance of follocular dendritic cells in a subject and for altering the architecture of the organs of the immune system. The method is useful for treating tumours, specifically follicular lymphomas. It offers an alternative therapy for those with tumours resistant to traditional chemotherapy. The present sequence represents the extracellular region of the human LTbeta-receptor and comprises the ligand binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour necrosis factor receptor LTbR protein SEQ ID NO:6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 197;
                                                                                                                                                                                                                                                                                  New method of treating follicular lymphomas by inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                            interaction between lymphotoxin-beta and its receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1133; DB 20
100.0%; Pred. No. 6.7e-84;
ive 0; Mismatches 0;
                                                                                                                                                      Tsiagbe V;
                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 25-26; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36700 standard; Protein; 415 AA.
98US-0073410.
98US-0073112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TTCKNPLEPLPPEMSGT 197
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Best Local Similarity 100.0
Matches 197; Conservative
                                                                                                                                                                                                                    WPI; 1999-469242/39.
                                                                                           (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200071150-A1.
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   02-FEB-1998;
30-JAN-1998;
                                                                                                                                                         Browning J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2001
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New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflammation
                                            Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host disease; skin allergic reaction; immune complex disease; malaria; transplantation rejection.
               TNF-R extracellular Cys-rich domain TNF-R-rp.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1; 78pp; English.
                                                                                                                                                                                                                                                                           (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                or autoimmune diseases
                                                                                                                                                                                                                                                                                                                                      WPI; 1999-080781/07.
                                                                                                                         Homo sapiens
                                                                                                                                                    W09853842-A1
                                                                                                                                                                                                               29-MAY-1998;
                                                                                                                                                                                                                                             30-MAY-1997;
                                                                                                                                                                                  03-DEC-1998.
                                                                                                                                                                                                                                                                                                         Greene MI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor.

Creceptor 5 (TRNF-5 or TR5). TRID has cytostatic, immunosuppressive, noctropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful in the treatment of tumours, resistance to polynuclocideotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restlenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and cortain haematopoietic cells, to regulate antiviral responses and gonist or TRAIL binding facilitator. The antibodies which bind TRID colypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID colypetides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; or useful in the diagnosis, treatment or prevention of: (a) cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                            Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%; Score 771; DB 22; Length 415; 70.7%; Pred. No. 2.1e-54;
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                                                                                                                                                                                                                                                           Disclosure; Fig 2; 285pp; English
                                                                                                                                      'n
                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                          18-MAY-2000; 2000WO-US13515.
                                                                        99US-0135164.
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                                                                                                                                                                 WPI; 2001-041051/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1999
                                                                        20-MAY-1999;
              30-NOV-2000.
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                                                                                                                                    Wei Y,
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Murali R, Takasaki W;

98WO-US10891

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The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNR-R) superfamily member. The compounds are especially designed from a binding loop of TNR-R p55. They are capable of inhibit the biological activities of TNR-R p689 may be used to inhibit the biological activities of TNR-They may be used in treating TNR-associated conditions such as acute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease,
                                                                                                                                                                                                                                                                                         transplantation rejection and malaria. Administration is, e.g. oral, transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-itch domain of TNF-R from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 VCATCAENSYNEHWNYLTICOLCRPCDPVMGLEEIAPCTSKRKTOCRCOPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human INF-R extracellular Cys-rich domain INF-R-rp SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.2%; Score 456; DB 20;
100.0%; Pred. No. 9.2e-30;
live 0; Mismatches 0;
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100.08; Pre
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Matches 77; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antinflammatory and immunomodulatory activities, and are tumour necrosis factor (TNF) related activation induced cytokine (TRANCE)/ receptor activator of NF-kappaB ligand (RANK) inhibitors. The method is useful for treating diseases characterised by bone loss such as osteoporosis, Paget's disease, and modulating dendritic cell maturation, T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor receptor (TNR-R) superfamily member, which is used in the exemplification of the present invention.
osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic; antirheumatic; antiarthritic; antiinflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of a recombinant human (rhu) tumour necrosis factor receptor {\tt TNFR/fc} fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides and peptide analogs which are TRANCE/RANK inhibitors
                                  receptor activator of NF-kappaB ligand; RANK; osteoporosis; Paget's disease; metastatic bone disease; rheumatoid arthritis; periodontal disease; modulating dendritic cell maturation; T cell proliferation; CD40 receptor system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for inhibiting
                                                                                                                                                                                                                                                                                                                                        for inhibiting osteoclastogenesis and bone resorption
                                                                                                                                                                                                                                                                               Murali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.2%; Score 456; DB 22;.
100.0%; Pred. No. 9.2e-30;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                               Greene MI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR51003 standard; Protein; 518 AA.
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                               Baron R,
                                                                                                                                                                      28-JUL-2000; 2000WO-US20510.
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                                                                                                                                                                                                                  UYPE-) UNIV PENNSYLVANIA.
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                                                                                                                                                                                                                              AOKI K.
HORNE W C.
BARON R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                               Horne WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AA;
                                                                                                                       WO200108699-A1
                                                                                                  Homo sapiens.
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                                                                                                                                                                                            28-JUL-1999;
                                                                                                                                              08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                       BARO/)
                                                                                                                                                                                                                                            HORN/)
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                                                                                                                                                                                                                                                                                                                             Jo est
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AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast

cell line WI-26 VA4. The mature full-length TWFRI is a glycoprotein
having a mol. Wt. of about 75-80 kDa The cloning of the cDNA for
TWFRI was described in Smith et al., Science 248:1019,1990. Clone 1
is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A
recombinant chimeric antibody may be produced having TWFR sequences
substituted for the variable domains of either or both of the
immunoglobulin molecule heavy and light chains and having
contained for the variable domains. A specific example of a TWFR/FC
immunoglobulin molecule heavy and light chains and having
contained for the variable domains. A specific example of a TWFR/FC
inston protein is given in AAQ4525/K51003. The rhu TWFR:FC fusion
gene was created by ligating the following fragments into a cloning
vector: 1) an 867 bA ARPIBS-PVUZ fragment from pCAV/NOT-TWFR (ATCC
68088) contg. the cDNA encoding the truncated TWFR. 2) a 700 bp
styl-Spel fragment from plasmid pIXX498 coding for 232 AAs of the
copyrion of human IgG1: Plasmid pIXX498 is a yeast expression
vector contg. the FC fragment of human IgG1: 3) An oilgo linker; to
fuse the truncated TWFR with the human IgG1: PC fragment. This
cond of the truncated TWF receptor and the 5' end of human IgG1.

Cand primer AAQ45227, which is an antisense sequence encoding bps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 kcrpgfgvarpgtetsdvv----ckpcapgtfsnttsstdicrphqicn---vvaip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating TNF mediated inflammatory diseases with TNF antagonist esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 518;
necrosis factor receptor; chimeric antibody molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.8%; Score 315; DB 15;
35.5%; Pred. No. 1.5e-17;
ive 24; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 32-34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gnasmdavctstsptrsmap 240
                                                                                                                                                                                                                                                                                                                               93WO-US08666
                                                                                                                                                                                                                                                                                                                                                                                                  92US-0946236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human IgG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMY ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-118172/14.
N-PSDB; AAQ45225.
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                                     immuglobulin
                                                                                                                                                                                                                                                                                                                               14-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1992;
                                                                                                                                                                                  WO9406476-A.
                                                                                                                                                                                                                                                            31-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs CA,
                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 lwnwvpeclscgsrcssdgv----etgactregnrictcrpgwycalskgegcrlcaplr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the region of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane may be used in the production of a pharmaceutical composition for increasing the inhibitory effect of a soluble receptor of the TNF/NGF receptor family. This sequence is the sequence of the p75 TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 aftpyapepgstcr--lreyydqtaqmccskcspgqhakafctktsdtvcdscedstytq 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor (TNF) receptor ligand - used to increase inhibitory effect of a soluble TNF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                         Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%; Score 309; DB 16; Length 461; 35.5%; Pred. No. 4e-17; 1ive 24; Mismatches 77; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Indels
                                                                                                                                                                                                                                                                                                  /note= "Unidentified amino acid."
                                                                                                                                                                                                                                                        258..285
/label= Transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p75 Tumour Necrosis Factor Receptor.
                                                                                                                                                                                                             Cocation/Qualifiers
27..214
/label= TBPII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Figure 2; 18pp; English.
                          AAR72504 standard; Protein; 461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mett I,
                                                                                                                                                                                                                                                                                                                                                                                                                                               RES & DEV CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                      94EP-0116015.
                                                                                                                                                                                                                                                                                                                                                                                                                  93IL-0107267.
                                                                                  (first entry)
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Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beletsky I, Bigda J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-148673/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & (WALL/) WALLACH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ89544.
                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                    Homo sapiens.
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                                                                                  31-OCT-1995
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                                                                                                                                                                                                                                                                                                                              EP648783-A.
                                                      AAR72504;
                                                                                                                                                           receptor.
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                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                        Domain
             AAR72504
RESULT
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The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL; human CC chemokine HCC5; human deubiquitinating proteins Dubl1 and Dub 12; human Mo-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proteins which are important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or be used for treating medical conditions and as immune, inflammatory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function, AAY77462 and AAY77481 are rodent proteins of undefined function, and AAY77482 is an avian protein of undefined function. These sequences are given in the sequence listing but are not referred to in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergic disorders, or abnormal cellular proliferation, for example, cancers or degenerative conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnston JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell memory play an important role. Sequences AAY77463-Y77464,
AAY77474-Y77475 and AAY77484 represent primate proteins of undefined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated mammalian genes, used to develop products for treating e.g. immune, inflammatory or allergic abnormalities, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune thyroiditis, as well as acute and chronic inflammatory responses in which T cell activation, expansion, and/or immunologism
                                                                                                                                                           Imune disorder; inflammation; allergy; immunosuppressant;
antiarthritic; antirheumatoid; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorman DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EE, Mattson JD, Gorman
Murgolo NJ, Greene JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 170-171; 218pp; English.
                                                                                                                     Primate protein sequence, SEQ ID NO:14
AAY77463 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lees EM;
                                                                                                                                                                                                                                                                                                                                                                                                    98US-0110938.
98US-0114466.
98US-0093897.
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98US-0136214.
98US-0099999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degenerative conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hedrick JA, Wang L,
Bazan JF, Mahony D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-171015/15.
                                                                                                                                                                                                                                                                                 WO200001817-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-1998;
18-AUG-1998;
11-SEP-1998;
                                                                           05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999;
                                                                                                                                                                                                   antithyroid
                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-1998;
23-JUL-1998;
                                                                                                                                                                                                                                                                                                                        13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998
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                                     AAY77463;
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Best Local Similarity
Matches 70; Conserv
                                                                                                                                       · 227 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9824463-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bendele AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 - JAN - 1997
                                                                                                                                        Sequence
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                                                               multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute panoreatitis; Alzhelmer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an ostooprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha -
                                                                                                                                        64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                            141
                                                                                                                                                                                              DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                  85
                                                                           Gaps
                                                                                              5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                      Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
                                                                                                                                                    aftpyapepgstcr--lreyydqtaqmccskcspgqhakvfctktsdtvcdscedstytq
                                                                          28;
                                                    Length 225;
                                                                          Indels
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                                                         4e-17;
                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang M,
                                                               Pred. No. 4e-1
24; Mismatches
                                                     Score 305;
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the remainder of the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 316pp; English.
                                                                                                                                                                                                                                                                                                   AAB66981 standard; Protein; 227
                                                                                                                                                                                                                           GTAQSDTTC -- KNPLEPLPP 192
                                                                                                                                                                                                                                               gnasmdavctstsptrsmap 211
                                                   26.9%;
35.0%;
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lacey DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-103031/11.
                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                     225 AA
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                                                                                                                                                                                                                                                                                                                                                                  Infr2 protein.
                                                                                                                                                                                                                                                                                                                                              19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-DEC-1999;
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                                                                          70;
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                                                                                                                                                                                                                                                                                                                         AAB66981;
                     Sequence
                                                    Query Match
                                                                                                                                                                                                                                               192
                                                                                                                  28
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                                                                          Matches
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, fibroblast growth factor (FGF)1-10 modulators and/or platelet factor (PAF) antagonists. The method is useful for treating
                                                                                                                                                                                                                                 atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock. The present sequence was used in a sequence
                                  activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclenosis, osteoprosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus earthematosus (SLE) an graft versus-host disease (GYHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 lwnwvpeclscgsrcssdqv----etqactreqnrictcrpgwycalskgegcrlcaplr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AVPPYASE-NOTCRDOEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour necrosis factor; TNF; TNF receptor type II; inflammatory disease; leukaemia; TNF binding protein; anti-inflammatory drug; methotrexatess.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human soluble tumour necrosis factor receptor type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.9%; Score 305; DB 22
35.0%; Pred. No. 4.1e-17
iive 24; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sennello RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW59665 standard; Protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GTAQSDTTC - - KNPLEPLPP 192
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96US-0032587.
97US-0036355.
97US-0039315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-333039/29.
N-PSDB; AAV41549.
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Boyle WJ, Wooden S;
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                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                           235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35-NOV-1998.
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                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease; tumour necrosis factor binding protein; autoimmune disease; arthritis; adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy; tumour necrosis factor inhibitor; Alzheimer's disease; TNBP.
                                                                                                                                                                                                                         HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                     DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                     This is the amino acid sequence of the human tumour necrosis factor receptor type II, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.
                                                                                                                                                                                  5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Truncated and soluble forms of tumour necrosis factor receptor - useful for treating diseases involving factor, e.g. arthritis and adult respiratory distress syndrome
                                                                                                                                26.9%; Score 305; DB 19; Length 235; 35.0%; Pred. No. 4.2e-17; ive 24; Mismatches 78; Indels 28
one additional anti-inflammatory drug, e.g. methotrexate
                                                                                                                                                                                                                                                                                                                                                                 AAW52270 standard; Protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kieft GL;
                    Disclosure; Fig 2; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor inhibitor.
                                                                                                                                                                                                                                                                                            GTAQSDTTC -- KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                gnasrdavctstsptrsmap 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0039792.
96US-0021443.
96US-0032534.
97US-0037737.
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                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fisher
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                                                                                                                                          Similarity
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                                                                                                  235 AA;
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                                                                                                                                    Local Sim.
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09-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                     AAW52270;
                                                                                                  Sequence
                                                                                                                                 Query Match
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                                                                                                                                         Best Loca
Matches
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This sequence is the human tumour necrosis factor inhibitor. The protein was used to make the truncated soluble tumnour necrosis factor receptor (gTNFR) proteins of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cacheria/Anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Calls transformed with a vector containing DNA encoding the protein may be used for production of recombinant sTNFR, which may also be used for measuring the amount of STNFR in samples and to raise antibodies against STNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The STNFR proteins are well suited to large scale production (since they lack the demindation site in region 11-126, so are more stable in yivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 305; DB 19;
Pred. No. 4.2e-17;
4; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fumour necrosis inhibitor 40 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW89234 standard; Protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
3; Fig 8; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GTAQSDTTC -- KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gnasrdavctstsptrsmap 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.9%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPG; chimeric; fusion; dinflammation; apoptosis.
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an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated Al monomers; (2) an isolated nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNF)/OPG chimeres are used to treat TNF and TNFF, mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The fused heterologous sequences to identify potential new receptors with flands. The present sequence represents the TNF inhibitor 40 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                     present invention describes a chimeric polypeptide (A1), comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * 5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p75 tumour necrosis factor receptor; mutant; PEG conjugated protein; polyethylene glycol conjugation; PEG conjugation; protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a K108R mutant of soluble p75 TNF receptor.
            New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "wild type Lys replaced with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.9%; Score 305; DB 20; 35.0%; Pred. No. 4.2e-17; ive 24; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
108
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                                                                                   Disclosure; Fig 3; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                  protein.
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The present sequence represents a N-terminal fragment of a mutant of the soluble tumour necrosis factor (TNF) receptor, where the wild the soluble tumour necrosis factor (TNF) receptor, where the wild of type to state the space of the soluble tumour necrosis factor (TNF) receptor and ligand. These residues are also potential polyethylene glycol (PEG) conjugation after some the profession of the invention. The specification describes a method for conjugating proteins with PEG to result in PEG conjugated proteins having little or no reduction in a desired activity. Specifically, one or more amino acid residues that are critical for protein bioactivity and which are capable of reacting the methods provide PEG conjugated proteins that are more homogeneous and present in higher yields. Conjugation does not take place at amino acid residues that are are critical to the proteins bioactivity, thus maintaining the activity of the protein. The methods are used to produce PEG conjugated proteins. The methods are used to produce PEG conjugated proteins.
                                                                                                                                                                            Novel methods for site-specific protein modification by mutagenesis by replacing polyethylene glycol reacting sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 lwnwvpeclscgsrcssdqv----etqactreqnrictcrpgwycalsrqegcrlcaplr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p75 tumour necrosis factor receptor; mutant; PEG conjugated protein; polyethylene glycol conjugation; PEG conjugation; protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wild type N-termnal fragment of the soluble p75 TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 305; DB 21;
Pred. No. 4.2e-17;
4; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY54443 standard; Protein; 235 AA.
                                                                                                                                                                                                                                  Claim 17; Page 29; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.9%; Sco
35.0%; Pre
tive 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 GTAQSDTTC--KNPLEPLPP 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                          WPI; 2000-160577/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 70; Conserva
                                                                                                                                             N-PSDB; AAZ45759
               22-JUN-1998;
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                                                                                        Pettit DK;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                         tumour necrosis factor (TNE) receptor. The wild type Lys residues at positions 108 and 120 are replaced with Arg (see AAY5441-42). Lys120 and Lys108 make contact between the p75 receptor and ligand. These residues are also potential polyethylene glycol (PEG) conjugation sites. The wild type p75 TNF receptor protein was mutated and conjugated to PEG, using the method of the invention. The specification descries a method for conjugating proteins with PEG to result in PEG-conjugated proteins with PEG to result in PEG-conjugated proteins with PEG to result are critical for protein bioactivity and which are capable of reacting with PEG sites are deleted, prior to conjugation of the protein to PEG. The methods provide PEG conjugation does not take place at amino and present in higher yields. Conjugation does not take place at amino caid residues that are critical to the proteins bioactivity, thus maintaining the activity of the protein. The methods are used to produce PEG conjugated proteins. The methods are used to produce PEG conjugated proteins. The methods are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                           Novel methods for site-specific protein modification by mutagenesis by replacing polyethylene glycol reacting sites \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; {\rm LL}{-1}; inflammatory disease; degenerative disease; human; lymphotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||| | ||| :||: ::||: || aftpyapepgstcr--lreyydqtaqmccskcspgqhakvfctktsdtvcdscedstytq 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                               The present sequence represents a N-terminal fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%; Score 305; DB 21; Length 235; 35.0%; Pred. No. 4.2e-17; ive 24; Mismatches 78; Indels 2
                                                                                                                                                                                                                                    Claim 16; Page 35-36; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB37685 standard; Protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GTAQSDTTC -- KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 gnasmdavctstsptrsmap 189
                                        99WO-US13953
                                                                   98US-0102530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 40 kDa TNF inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Conservative
                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                                 WPI; 2000-160577/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA;
                                                                                                                                                                 N-PSDB; AAZ45762
                                        18-JUN-1999;
                                                                   22-JUN-1998;
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             29-DEC-1999
                                                                                                                          Pettit DK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 aftpyapepgstcr--lreyydqtaqmccskcspgqhakvfctktsdtvcdscedstytq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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                                                                                                                                                                                                                                                                                                                                         Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
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Pred. No. 4.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.9%; Scor...
35.0%; Pred. No. 4...
... 24; Mismatches
                                                                                                                                                                                                                                                                                                                                         Brewer MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4, 2002, 10:12:22
                                                                                                                                                                                                                                                                                                                                      King MW, Hale KK, Brewei
RW, Vannice J, Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Fig 38; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                               93US-0090366.
89US-0381080.
89US-0450329.
90US-0479661.
                                                                                            95US-0375242.
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Matches 70; Conservative
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Job time: 85 sec
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-006443/01
                                                                                                                                                                                                                                                                                       INC.
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                                                                                                                                                                                                                                                                                                                                                               Vanderslice RW,
                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN
US6143866-A.
                                                                                         19-JAN-1995;
                                                                                                                                         19-JUL-1990;
                                                                                                                                                                    09-JUL-1993
                                                                                                                                                                                     18-JUL-1989
11-DEC-1989
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                                               07 - NOV - 2000
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Sequence Sequence Sequence S

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Sequence

Sequence Sequence

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Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Seq

Sequence:

Run on:

Searched:

Database

Result 8. Sequence Sequence

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Sequence 1, Application US/08505606
Patent No. 5925351
GENERAL INFORMATION:
APPLICANT: BROWING, Jeffrey L.
APPLICANT: BROWING, Jeffrey L.
APPLICANT: HOCHMAN, Paula S.
TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTE TOTAL STATE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,606
FILING DATE: 21-JUL-1995
CLASSIFICATION: 424
US-08-794-796-2
US-08-996-139-15
US-09-996-139-15
US-09-015-649A-15
US-09-041-886-27
US-09-041-886-27
US-09-041-886-27
US-09-018-529-17
US-08-996-139-4
US-08-995-659-4
US-08-995-659-2
US-08-995-139-2
US-08-995-139-6
US-08-995-659-6
US-08-995-659-6
US-08-996-139-6
US-08-995-659-6
US-08-995-659-6
US-08-995-659-6
US-08-996-139-6
US-08-995-659-6
US-09-215-649A-6
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: James F. Haley, Jr.
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378,968
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27,794
SR: B191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: HALEY, Jr., James F. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 197 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
   ; MOLECULE TYPE: peptide US-08-505-606-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: U.S.A.
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   STRANDEDNESS:
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CITY: New
STATE: Ne
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  US-08-505-606-1
   (without alignments)
359.629 Million cell updates/sec
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Sequence 6, Appli
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Sequence 5, Appli
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                                                                                                                                    US-09-299-139A-1
1133
1 SQPQAVPPYASENQTCRDQE......QSDTTCKNPLEPLPPEMSGT 197
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                                                                                       Search time 13.38 Seconds
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.: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

.: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

.: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

.: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

.: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
              version 4.5
- 2000 Compugen Ltd.
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US-08-974-022-48
US-08-795-445A-48
US-08-795-447A-48
US-08-795-446B-48
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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US-09-042-785A-7
US-08-477-347-3
US-09-006-353A-4
US-08-476-862-2
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US-09-286-529-20
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US-08-385-229-2
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                                                                                                                                                                                                                          231628 seqs, 24425594 residues
                                                                                     4, 2002, 10:10:57;
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Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
              GenCore
Copyright (c) 1993
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length: 2000000000
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Match Length
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Maximum DB seq
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Perfect score:
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61 YNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL 118
                                                                                52 VCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE 111
                                                                                                                                                                                                                                                     Sequence 3, Application US/08866545
Patent No. 626535
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Murali, Ramachandran
APPLICANT: Takasaki, Wataru
TITLE OF INVENTION: PEPTIDES AND PEPTIDE
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 SDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.2%; Score 456; DB 4; 100.0%; Pred. No. 2.7e-36; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      009113-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/866,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFRENCE/POCKET NUMBER: 0091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,742
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MOLECULE TYPE: No. 6265535e
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LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 30-MAY
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208 SDTICKNPPEP 218
                                                                                                                                        SDTTCKNPLEP 189
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Best Local Similarity
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COUNTRY:
                                                                                                                                                                                                                                              US-08-866-545-3
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                                   Gaps
                                                                                     1 SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
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Length 197;
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                                   Indels
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APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR
WUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: HUMAN GENOME SCIENCES, INC.
100.0%; Score 1133; DB 2;
100.0%; Pred. No. 1.2e-99;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09006353A Patent No. 6261801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/OCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-6504
TELEFAX: (301) 309-6512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36,373
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NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                181 TICKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                              181 TTCKNPLEPLPPEMSGT 197
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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CLASSIFICATION: 435
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Best Local Similarity
Matches 135; Conserv
                 Similarity
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                 Best Local Sim
Matches 197;
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   Query Match
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64 HWNYLTICQLCR----PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
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                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
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Pred. No. 1.6e-21;
4; Mismatches 78
                          APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOYLO, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
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Sequence 48, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
                                                                                                                                  ADDRESSEE: Amgen Inc.
STREEF: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/577,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 35.0%;
Matches 70; Conservative 24
      Lacey, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 227 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-795-445A-48
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                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
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        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 227;
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Live 24; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
                                                                                                                                                                 APPLICANT: BOYJE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/974,022
12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 48, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                        Sequence 48, Application US/08974022
Patent No. 6015938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GTAQSDTTC -- KNPLEPLPP 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
'LENGTH: 227 amino acids
TYPE: amino acids
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Best Local Similarity 35.09
Matches 70; Conservative
61 CTHCELLSDCPPGTEAE 77
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                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                             US-08-974-022-48
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64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                       Length 227;
                                                                                                                                                                                                                                                                                                                       26.9%; Score 305; DB 4; Length 22' 35.0%; Pred. No. 1.6e-21; Live 24; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITILE OF INVENTION: OSTEOPROTECERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/795,446B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/08795446B Patent No. 6288032
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                               NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNASRDAVCTSTSPTRSMAP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 amino acids
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                                                                                                                                                                                                       single
                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-186-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
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Best Local Similarity
Matches 70; Conserva
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ZIP: 91320-1789
                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-795-446B-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKISDTVCDSCEDSTYTQ 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.9%; Score 305; DB 4; Length 227; 35.0%; Pred. No. 1.6e-21; Live 24; Mismatches 78; Indels
                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTLN RELEASE #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/974,186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Amgen Inc.
: 1840 Dehavilland Drive
Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-974-186-48
; Sequence 48, Application US/08974186
; Patent No. 6284740
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                 COMPUTER: IBM PC compatible
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: P.
INFORMATION FOR SEO ID NO: 48:
SEQUENCE CHARACTERISTICS:
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                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                            : 227 amino acids
amino acid
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Best Local Similarity 35.vv.
70, Conservative
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MOLECULE TYPE: protein
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CLASSIFICATION: 514
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ADDRESSEE: Amgen Inc
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COUNTRY: USA
ZIP: 91320-1789
  California
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                                       91362-1789
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                                                                                                                                                                                                                                                                                                                                          LENGTH:
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235 amino acids
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 LENGTH:
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                                                                                                                                                                                                                  5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Edwards, Carl K,
TITLE OF INVENTION: COMBINATION THERAPY USING A TWE BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING TWF-MEDIATED DISEASES
                                                                                                                       26.9%; Score 305; DB 4; Length 227; ilarity 35.0%; Pred. No. 1.6e-21; Conservative 24; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFERMY APPLICATION NUMBER: US/09/13/0 Version #1.30 CURENY APPLICATION DATA:
FILING DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICK APPLICATION DATA:

APPLICATION NUMBER: US 60/032,587
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
*FILING DATE: 23-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/052,023
FILING DATE: 09-UDL-1997
ATORNEY/AGENT INFORMATION:
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08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-326-394-4; Sequence 4, Application US/09326394; Patent No. 6306820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
                                                                                                                                                                                                                                                                                                                                                                                                                  175 GTAQSDTTC--KNPLEPLPP 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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                  single
                                                   ; MOLECULE TYPE: protein US-08-795-446B-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                Query Match
Best Local Similarity
Matches 70; Conserv
amino acid
                                    linear
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               STRANDEDNESS:
TOPOLOGY: lin
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Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      64 LWNWVPECLSCGSRCSSDQV----ETQACTREONRICTCRPGWYCALSKQEGCRLCAPLR 119
                                                                                                                                                                                                                                                                                                                                     64 HWNYLFICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                   120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 63
                                                                                                                                                                                                                                     5 AVPPYASE-NOTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                        Query Match 26.9%; Score 305; DB 4; Length 235; Best Local Similarity 35.0%; Pred. No. 1.6e-21; Matches 70; Conservative 24; Mismatches 78; Indels
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wight, Christopher L. REGISTRATION NUMBER: 31,680 REFERENCE/DOCKET NUMBER: 25 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 GNASRDAVCTSTSPTRSMAP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GTAQSDTTC--KNPLEPLPP 192
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TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 amino acids
amino acid
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-326-394-4
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STATE: Washington
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                       86 LWNWVPECLSCGSRCSSDOV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFSNTTSSTDICRPHQICN----VVAIP 191
                                                                                                                                                                                                              28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
                                                                                                                                                                    5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
26.9%; Score 305; DB 1; Length 461; 35.0%; Pred. No. 3.4e-21; Live 24; Mismatches 78; Indels
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Thore is the company of th
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY AGENT INFORMATION:
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ER: 2501-D
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STREET: 51 University Street
CITY: Seattle
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REPERENCE/DOCKET NUMBER: 2501
TELECOMMUNICATION INFORMATION:
TELEFRAX: (206) 287-0430
INFORMATION FOR SEQ ID NO: 2:
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                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                          Local Similarity
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STATE: Wash
COUNTRY: U.
ZIP: 98101
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        Query Match
                                              Best Loca
Matches
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64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BUSIGLED, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCES:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                5 AVPPYASE - NOTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                              28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
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                                                                                                         Length 461;
                                                                                                                                                     78; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
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Pred. No. 3.4e-21;
                                                                                                         26.9%; Score 305; DB 2;
35.0%; Pred. No. 3.4e-21;
Live 24; Mismatches 78
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MEI-001CP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GTAQSDTTC--KNPLEPLPP 192
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35.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
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                                                                                                         Query Match
Best Local Similarity 35.09
Matches 70; Conservative
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                ; MOLECULE TYPE: protein US-08-650-000-2
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity
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; FRAGMENT TYPE:
US-09-042-785A-7
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86 LWNWVPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
                                                                           64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                       64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
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                         28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
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 5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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35.0%; Pred
tive 24; I
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NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                                                                                                                                                                  192 GNASMDAVCTSTSPTRSMAP 211
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WEL, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR
NUMBER OF SEQUENCES: 26
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Best Local Similarity 35.0%
Matches 70; Conservative
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COMPUTER READABLE FORM:
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STATE: M
COUNTRY:
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                                                                                                            HWNYLTICQLCR----PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                    120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
 Gaps
                                                                                                                                                                                                             Gaps
                                                            28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQ 85
                                      5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
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   Indels
 78;
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35.0%; Pred. No. 3.4e-21;
ive 24; Mismatches 78;
 24; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 Seventh Street, N.W
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APPLICATION NUMBER: 08/115,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: BELETSKY, Igor
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08477347
Patent No. 6232446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                175 GTAQSDTTC--KNPLEPLPP 192
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INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WALLACH, David
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amino acid
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 Conservative
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Best Local Similarity
Matches 70; Conserv
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APPLICANT: WALLACT
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70;
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120 DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                            5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20004
ZONPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: THE INHIBITORS NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 419 Seventh Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 1899
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                    RESULT 15
US-08-476-862-2
Sequence 2, Application US/08476862
Patent No. 6262239
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELFISKY, IGOT
APPLICANT: METT, IGOT
APPLICANT: ENGELMANN, HARTMUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-737-3520
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                 175 GTAQSDTTC--KNPLEPLPP 192
                                                                                                                        192 GNASRDAVCTSTSPTRSMAP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
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us-09-299-139a-1\_1.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 4, 2002, 10:10:57; Search time 19.61 Seconds · (without alignments) 965.303 Million cell updates/sec

Run on:

Title: Perfect score: Sequence:

US-09-299-139A-1 1133 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	fumor nearest at the fact of t	necrosis fa		ε	B-cell activation	B cell-associated	death receptor-6 -	OX40 antigen precu	ox40 pro	tumor necrosis fac	hypothetical prote	qene G4R protein -	G2R protein - vari	tumor necrosis fac	OX40 homolog - hum	tumor necrosis fac	CD30 antigen precu	lymphocyte activat	TŽ protein - rabbi	a)	tumor necrosis fac	T2 protein - myxom	apoptosis-mediatin	T-cell antiqen 4-1	nerve growth facto	membrane glycoprot	nerve growth facto	apoptosis-mediatin	nerve growth facto
SUMMARIES		T54182	A35356	B38634	148854	A60771	A46476	JC7705	S12783	148700	GQHUT1	T28623	D36858	D72175	JC4302	137552	GQMST1	A42086	138426	B43692	I37383	GQRTT1	GQVZML	A40036	B32393	A26431	JC5486	JN0006	A46484	GQHUN
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di	Query Match		26.9	26.0		24.5	21.5	20.0				18.5					17.7	17.3	17.3	16.7	16.5	16.3	16.2	16.0	15.8		14.7	14.5	14.3	13.1
	Score	1133	305	295	290	278	243.5	226.5	222.5	214.5	210.5	210	210	207	206	201	201	196	195.5	189	187.5	184.5	183.5	181	179.5	171.5	166	164	162	148.5
	Result No.	-	7	ю	4	5	9	7	æ	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990

qq

Fas antigen precur	CD27 antigen precu	hypothetical prote	hypothetical prote	laminin alpha-1 ch	furin (EC 3.4.21.7	cysteine rich prot	laminin alpha 5 ch	hypothetical prote	subtilisin-like pr	subtilisin-like pr	heparan sulfate pr	furin (EC 3.4.21.7	Delta-4 protein -	DELTA-like 1 - mou	subtilisin-like pr
			. ,			-									
JC2395	A46517	T26972	T27283	MMMSA	T43251	T42017	T10053	T29764	G02428	JC6148	S18252	A43434	JC7569	148324	A48225
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324	260	1111	1620	3084	1299	1274	3635	2180	899	915	3707	1680	686	722	915
12.8	11.7	11.7	11.4	11.4	11.3	11.3	11.1	11.1	11.0	11.0	11.0	10.9	10.9	10.9	10.8
145.5	133	132.5	129.5	129	128.5	128	1.26	125.5	124.5	124.5	124.5	124	123.5	123	122.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Bibliand

Under necrosis factor receptor type 2 precursor - mouse
C;Species Nus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; 554816 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; 554816 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; 554816 50-Jun-1992 #text_change contains a contain a contains a contain a contain a contains a contain a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AVPPYASE - NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 PYASE-NOTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
F;164-201/Domain: NGF receptor repeat homology <nv4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;280-461/Domain: antracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 LWNWVPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 DCPPG-----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP
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                                                                                                                                                                                                                                                                                                                             26.9%; Score 305; DB 1;
35.0%; Pred. No. 5.4e-16;
iive 24; Mismatches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 GNASMDAVCTSTSPTRSMAP 211
                                                                                                                                                                                                                                                                                                                                   Query Match 26.9%,
Best Local Similarity 35.0%,
Matches 70; Conservative
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Best Local Similarity
Matches 66; Conserv
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A; Residues: 23-461 CDEM.
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra A; Accession: A36007; MUID:90349572
                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8311-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 116-140, P', 142-195, R', 197-362, T', 364-461 <HEL>
A; Residues: 116-140, P', MID: 9339751; PIDN: AAA63262.1; PID: 9339752
A; Cross-references: GB: M35857; NID: 9339751; PIDN: AAA63262.1; PID: 9339752
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
J. Biol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial amino acid sequence analysis of two distinct tumor ned
A; Reference number: A23666; MUID: 91056048
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A,Accession: 138094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA

A; Residues: 1-157, R', 197-461 (KOH)

A; Residues: 1-157, R', 197-461 (KOH)

A; Cross-references: GB:M55994; GB:M35549; NID:g339757; PIDN:AAA36755,1; PID:g339758

R; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990

A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular,

A; Reference number: A48416; MUID:91370690
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A Molecule type: protein
B Molecule type: protein type
B Molecule type

     A,Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A,Reference number: A35356, MUID:90260639
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C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <AMAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
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A;Molecule type: DNA
A;Residues: 1-37 <RES>
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A;Cross-references: GDB:125914; OMIM:191191
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Gene 150, 381-386, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A48416
A; Status: preliminary
A; Molecule type: mRNA; protein
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A Molecule type: protein
A Residues: 27-31 < ENG>
                                                                                                                                                                                                                                                                                 A; Residues: 1-461 <SMI>
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Gaps

20;

Length 474;

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A; Molecule type: protein A; Expedimental source: Burkitt lymphoma cell line Raji C; Genetics:
     A; Reference number: A60771; MUID:89093941
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                           C, Accession: 148854
R; Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                         121
                                                                            145
                                                                                                                 181
                                                                                                                                   67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 QFRICLSCSSCSTDQV----ETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT 181
   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PYKPEPGYECQISQ-EYYDRRAQMCCAKCPPGQYVKHFCNKISDIVCADCEASMYIQVWN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                        gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
                                                              90 QFRTCLSCSSCTTDQV----EIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKC
PYKPEPGYECQISQ-EYYDRKAQMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWN
                                   67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC
                                                                                                             122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%; Score 290; DB 2; 33.5%; Pred. No. 7.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: 148854
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 148854; MUID:95178848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:X76401;
C; Superfamily: tumor necrosis fac
F;151-188/Domain: NGF receptor re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 33.59
Matches 65; Conservative
                                                                                                                                                                                     182 TCKNPLEPLPPEMS 195
                                                                                                                                                                                                                           201 VC----APESPTLS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 TCKNPLEPLPPEMS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 VC----APESPTLS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-459 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
qq
                                   δ
                                                                    рp
                                                                                                           Qγ
                                                                                                                                                qq
                                                                                                                                                                                     δ
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A,Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen: NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein: surface antigen; transmembrane prot
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A46476

B cell-associated surface molecule CD40, long splice form - mouse

C; Species: Mus musculus (house mouse)
C; Accession: A46476; A46515
R; Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-625, 1992
A; Title: Differential increase of an alternatively polyadenylated mRNA species of mur A; Reference number: A46476; MuID:92105763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: M83312; NID:g1553058
A; Cross-references: GB: M83312; NID:g1553058
A; Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A; Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
A; Note: this translation is not annotated in GenBank entry HUSCD40A, release 113.0
B; Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay, J. Immunol. 149, 3921-3926, 1992
A; Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A; Reference number: A46515
A; Reference number: A46515
A; Reference number: compared with conceptual translation
A; Residues: 1-287, LW <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: M83312; NID:q1553058; PIDN: AAB08705.1; PID:q1553059; GB: M94126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 PPTA----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTETECLPCGESEFELDTWN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 PPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AELKDEVGKGNNHCVPCKAGHFQNTSSPŞARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 278; DB 2; Length 277;
Pred. No. 4e-14;
0; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                     F;194-215/Domain: transmembrane #status predicted <TWM>F;216-277/Domain: intracellular #status predicted <CYT>F;153,180/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: BALB/c, liver
A; Note: sequence extracted from NCBI backbone (NCBIP:120357)
C; Comment: For an alternative splice form, see PIR:A46515.
C; Comment: For an alternative splice form, see PIR:A46476.
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: alternative splicing; transmembrane protein
F; 105-144/Domain: NGF receptor repeat homology
                                    A; Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.5%; Scor
35.0%; Preditive 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-305 <TOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A; Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
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Length 305;

Score 243.5; DB 2; Pred. No. 1.7e-11;

21.5%; 31.0%;

Length 271;

DB 2;

Indels

85

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Jean court of protein - mouse

N; Alternate names: OX40 antigen

N; Alternate names: OX40 antigen

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: 148700; 148334; S34377

R; Calderhead, D.M.; Bullhann, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.

J; Immunol. 151, 5261-5271, 1993

A; Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell

A; Reference number: 148700; MUID: 94044750

A; Reference number: 148700

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-272 <RES>
A; Cross-references: EMBL: 221674; NID: 9312827; PIDN: CAA79772.1; PID: 9312828

R; Rirkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.

Eur. J: Immunol. 25, 926-930, 1995

A; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX

A; Reference number: 148334; MUID: 95255413

A; Residues: translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-14, 'G', 16-272 <RE2>
A; Cross-references: EMBL: X85214; NID: 9732818; PIDN: CAA59476.1; PID: 9732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 MGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------PGTQPR-QDSSHKLGVDC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 MGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHC 140
                                                                                                                                                                                                                                                                                                                                    21 KEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 KEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPV 80
                                                                                                                                                                                                                                                                                                                                                                   141 VPCKAGHFQNTSSP--SARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 VPCPPGHFSPGSNQA--CKPWTNCTLSGKQIRHPASNSLDIVCED 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 VPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
C; Superfamily: CD27 antigen; NGF receptor repeat homology C; Keywords: growth factor receptor; transmembrane protein F: 1-19/Domain: signal sequence #status predicted <SIG> F: 20-271/Product: 0X40 antigen #status predicted <AMXT> F: 211-235/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                        Query Match 19.6%; Score 222.5; DB 2
Best Local Similarity 32.1%; Pred. No. 6.1e-10;
Matches 53; Conservative 17; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.9%; Score 214.5; DB : 31.7%; Pred. No. 2.5e-09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 SGSELKONCTPTEDIVCOCR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 SGSELKONCTPTODIVCRCR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.7%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs tresia, activates a cell death and/or survival signaling cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 positive T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #status predicted <ECL>
      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  death receptor-6 - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Sate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C; Accession: JC7705
R; Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A; Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A; Reference number: JC7705; MUID:21308433; PMID:11414698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.Alternate names: nerve growth factor receptor homolog
C; Species: Rattus norvegicus (Norway rat)
C; Decies: Rattus norvegicus (Norway rat)
C; Decies: Rattus norvegicus (Norway rat)
C; Decies: Rattus norvegicus (Norway rat)
C; Accession: S12783; S08036
R; Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A; Title: Characterization of the MRC OX40 antigen of activated CD4 positive A; Reference number: S12783; MUID:90214614
A; Accession: S12783
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-271 cMAL>
A; Residues: 1-271 cMAL>
A; Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
                                                                                                                                                                                   RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG----TEAEL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTSKRKTQCRCQPGMF-----CAAWALECTHCELLSDCP-----PGTEAELKDEVGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 LICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCE--LPMIEKTH 107
                                                                                                                        25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH 80
         Gaps
                                                                TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCR-PCDPVMGLEEIAP 88
                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | || | | : | :| | :| | :| | | :| | | 199
DVRCKPCLRGTFSDVPSSVMKCKTYTDCFGKNMVVVKRGTKESDNVCXSP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 NNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNP 186
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Keywords: ovary
F:1-21/Domain: signal sequence #status predicted <SIG>
F:2-196/Domain: extracellular cysteine-rich, ligand-binding
F:32-196/Domain: extracellular estatus predicted <TrMM>
F:31-5/Domain: transmembrane #status predicted <DED>
F:410-475/Domain: death domain #status predicted <DED>
F:551-651/Region: conserved cytoplasmic #status predicted
      81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.0%; Score 226.5; DB 2; 28.8%; Pred. No. 6e-10; iive 26; Mismatches 62;
      Mismatches
      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AF349908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.09
Best Local Similarity 28.89
Matches 49; Conservative
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OX40 antigen precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-651 <BRI>
      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: dr-6
      Matches
                                                                15
                                                                                                                                                                                   75
                                                                                                                                                                                                                                             81
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S12783
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Length 272;

DB 2;

Indels

---PGTQPR-QDSGYKLGVDC 123

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A; Molecule type: protein
A; Residues: 41-45 < CMC>
A; Residues: 41-45 < CMC>
B; Residues: 41-45 < CMC>
B; Rajihara, J:; Asada, A.; Kirihara, S.; Kato, K.
B; Rajihara, J:; Asada, A.; Kirihara, S.; Kato, K.
B; Rajihara, J: Biochem. 58, 2266-2268, 1994
A; Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purifie
A; Reference number: JC2404; WUID:95128033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
30-211/Domain: extracellular #status predicted <EXT>
41-201/Product: TFF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat 44-83/Domain: NGF receptor repeat homology <NG1>
84-126/Domain: NGF receptor repeat homology <NG2>
A,Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequ
A,Reference number: A60231; MUID:90292116
                                                                                                                                                      A) Residues: 41-43, 7X, 45-53, 7X, 55-57 <SEC>
R)Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G. Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein fr A;Reference number: A60594; MUID:89171156
A;Accession: A60594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecules: 41 3, 'x', 45-53, 'v', 55-57, 'XK', 60 <0LS>.
A;Rolecules: 41 source: renal failure patient urine
B;Engelmann, H.; Novick, D.; Wallach, D.
D Biol. Chem. 265, 1331-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A;Reference number: A35010; MUID:90110215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Reywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <NEM>
F;215-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRHCLSCSKCKKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSL---CLNG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEAELKDEVGKGNNHCVPCKAGHF - - QNTSSPSARCQPHTRCENQGL - - VEAAPGTAQSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 LTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWA---LECTHCELLSDCPPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 DQEK-----EYYEPQHR-ICCSRCPPGTYVSAKC-SRIRDTVCATCAENSYNEHWNY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 DREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 41-53, X',55-144, X',146-150, X',152-186, X',188-201 <KAJ>
A; Residues: 41-53, X',55-144, X', 146-150, X',152-186, X', 188-201 <KAJ>
A; Experimental source: urine
C; Comment: This protein is one of two known receptors for both TNF-alp'
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 210.5; DB 1 Pred. No. 7.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
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                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A38258; MUID:91062364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Conservative
                                                                                                                        A; Molecule type: protein
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A38258
                                                                                 A; Accession: A60231
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        Nultenaerosis factor receptor 1 precursor (validated) - human
Nultenaerosis factor receptor 1 precursor (validated) - human
Nultenaerosis factor receptor 1 preceptor; Nr Preceptor type 1
Nr Contante themse PSD fund necrosis factor receptor; The receptor type 1
Nr Contante themse PSD fund necrosis factor receptor; The receptor type 1
Nr Contante in the same separated and same separated and the same separated and same separated same separated and same separated same separated and same separated same separated same separated same separated same separated
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A; Reference number: $12057; MUID:91006021
A; Accession: $12057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y:; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ne
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A;NOte: parts of soluble TNF binding protein 1, including its amino and carboxyl ends,
R;Kemper, O.; Wallach, D
Gene 134, 209-216, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Cloning and partial characterization of the promoter for the human p55 tumor A;Reference number: JT0758; MUID:94085779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.; Wingfield, P.; Dayer, J.M.
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A; Residues: 1-13 < KENA
B; Seckinger: P.; Vey, E; Turcatti, G
Eur. J. Immunol. 20, 1167-1174, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-455 <NOP>
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Gaps

23;

84; DB 1;

<del>..</del>

Length 455; Indels

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GSE protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shochelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo submitted to GenBank, March 1998
A;Bescription: Analysis of the complete coding sequence of DNA of alastrim variola mi A;Reference.number: A72150
A;Accession: D72175
A;Actus: preliminary
A;Molecule type: DNA
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759 A;Experimental source: strain Garcia-1966 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 LIICQICR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 LPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRACVSQTKC--GI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PYTPPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 PYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNY
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A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Coss-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Cene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGE>
F;88-109/Domain: NGF receptor repeat homology <NGS>
F;110-151/Domain: NGF receptor repeat homology <NGS>
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 2;
6.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYGVSGHTSVGDVICSPCGFGTYSHTVSSADKCEP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
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                                                                                                                                                                                                                                                                                                                                                                                                18.5%; Score 210; DB 29.0%; Pred. No. 6.5e Live 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Conservative
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-349 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                    C; Species: variola major virus
C; Species: variola major virus
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C; Accession: T28623
R; Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993
A; Title: Potential virulence determinants in terminal regions of variola smallpox virus
A; Reference number: 220488; MUID:94088747
A; Accession: T28623
A; Statuus: preliminary; translated from GB/EMBL/DDBJ
A; Statuus: DNA
A; Residues: 1-348 < AMS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A.Experimental source: strain India-1967, ssp. major, isolate Ind3
B.Kolykhalov, A.A.: Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol submitted to the EMBL Data Library, April 1992
A; Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P A; Reference number: $46868
A; Accession: $46888
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-349 < KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective A;Reference number: S32385, MUID:93202281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
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C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36658; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Reference number: D36858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
A;Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
      153 TVHLSCQE -- KQNTVCT-CHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 LPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKC--GI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 210; DB 2;
; Pred. No. 6.5e-09;
20; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 GYGVSGHTSVGDVICSPCGFGTYSHTVSSADKCEP 169
                                                                                                                                                                                                                                                                           hypothetical protein G2R - variola major virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: B28R protein (COP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.5%;
29.0%;
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Best Local Similarity 29.0%
Marches 45; Conservative
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A; Residues: 1-349 <BLI>
                                                                                                           210 TTVLLPL 216
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                                                                  181 TTCKNPL 187
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86 IAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKA 145
                                                                          -----TOPLDSYKPGVD------CAPCPP 130
                                                                                                                                 GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC--KNPLEPLPPEMSG 196
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                                                                          96 KOLCTATODIVCRCRAG-
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R; Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994
A; Title: The human Ox40 homolog: cDNA structure, expression and chromosomal assignment c A; Reference number: 137552; MUID: 94170844
                      R;Suter, B.; Pauli, U.
Gene 163, 263-266, 199.
A;Title: Cloning of the CDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645
                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor 1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;44-82/Domain: NGF receptor repeat homology <NG1>
F;44-126/Domain: NGF receptor repeat homology <NG5>
F;84-126/Domain: transmembrane #status predicted <TMM>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 TE----AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQ-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                         A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A;Accession: PC4093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 LTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWA---LECTHCELLSDCPPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 TVQLPCLEKQDTI-----CNCHSGFFLR----DKECVSCVNCKNADCKNLCPATSETR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQEK------EYYEPQHR-ICCSRCPPGTYVSAKC-SRIRDTVCATCAENSYNEHWNY 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.2%; Score 206; DB 2; 29.4%; Pred. No. 1.6e-08; iive 22; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.7%; Score 201; DB 2; 28.3%; Pred. No. 2.6e-08; ive 21; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                        A;Wolecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 29.44
Matches 57; Conservative
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202 NDFQDTGTTVLLPL 215
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C; Accession: JC4302; PC4093
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Best Local Similarity
                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-461 <SUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0x40 homolog - human
                                                                                                                              Accession: JC4302
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                           C; Genetics
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: October 4, 2002, 10:11:22 ; Search time 11.94 Seconds (without alignments)
638.840 Million cell updates/sec
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Title: US-09-299-139A-1
Perfect score: 1133
Sequence: 1 SQPOAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

-	Description	P36941 homo sapien	P50284 mus musculu	P20333 homo sapien	mus	O35305 mus musculu	homo	homo	3 bos t	P27512 mus musculu	Q92956 homo sapien		P47741 mus musculu	P19438 homo sapien		P50555 sus scrofa	pos	P43489 homo sapien	P25118 mus musculu	homod		s sns		019131 bos taurus		. P29825 myxoma viru	P25445 homo sapien	P20334 mus musculu	P07174 rattus norv	m	6	9	8138	Q63199 rattus norv
SUMMARIES	ID	N.	TNR3_MOUSE	TRIB_HUMAN	TRIB_MOUSE	TR11_MOUSE	TNR5_HUMAN	TR11_HUMAN	TNR5_BOVIN	TNR5_MOUSE	TR14_HUMAN	TNR4_RAT	TNR4_MOUSE	TR1A_HUMAN	VC22_VARV	TR1A_PIG	TNR6_BOVIN	TNR4_HUMAN	TR1A_MOUSE	TNR8_HUMAN	TNR9_HUMAN	TNR6_PIG	VT2_SFVKA	TR1A_BOVIN	TRIA_RAT	VT2_MYXVL	TNR6_HUMAN	TNR9_MOUSE	TR16_RAT	T10B_HUMAN	TR16_CHICK	TNR6_MOUSE	TR16_HUMAN	TNR6_RAT
	DB	П	Н	Н	Н	-	Н	-	Н	Н	-	-	Н	Н	-	-	Н		-	~	1	<b>-</b>	Н	Н,	<b>-</b> -	-	-	-	-4	Н	-	Н	Н.	-
	Length	435	415	461	474	625	277	616	269	289	283	271	272	455	349	461	323	277	454	595	255	332	325	471	461	326	332	256	425	440	416	327	427	324
æ	Query	100.0	68.0			25.0		24.4								٠.	٠.		17.7											14.8		14.3	13.1	12.8
	Score	1133	771	305	295	283	278	277	251.5	243.5	230.5	222.5	214.5	210.5	210	206	203	201	201	196	195.5	194	189	188	184.5	183.5	181	179.5	171.5	167.5	164	162	148.5	
	Result No:	П	7	e	4-	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	74	25	26	27	28	59	30	31	32	33

C00220 homo sapien 093038 h wsl-1 pro 015230 homo sapien P19137 mus musculu 02192 mus musculu 061001 mus musculu 097677 rattus norv 092824 homo sapien 09115 branchiosto 09155 mus musculu 097677 attus norv 092824 homo sapien 09185 hamofalosto 09135 drosophila
T10A HUMAN TR12_HUMAN LMAS_HUMAN LMA1_WOUSE TNR7_HUMAN LMAS_MOUSE LMAS_MOUSE DLL1_RAT PCK5_HUMAN PCK5_BRACL PGBM_MOUSE
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468 417 3695 3084 260 1799 3718 714 913 1696 3707
122.7 122.7 111.1 111.1 111.0 111.0 111.0
143.5 140.5 130. 129. 128. 126. 126. 124.5 124.5 124.5
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## ALIGNMENTS

DI DI	INKS_ROMAN STANDARD: PRT: 435 AA.	
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I L	01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence undate)	
5	(Rel. 40, Last annotatio	
a		osis factor receptor
DE	2 related protein) (Tumor necrosis factor C receptor). representation of managed.	eptor).
2 0	Homo garions (Himan)	
90	nomo sapiens (numan). Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	ata: Euteleostomi;
200	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo	idae; Homo.
XO		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Liver;	
RX	NE=93252381; PubMed=8486360;	
RA	Baens M., Chaffanet M., Cassiman J.J., den Bergh	den Berghe H., Marynen P.;
RT	"Construction and evaluation of a hncbNA library of human 12p	y of numan 12p
RT	transcribed sequences derived from a somatic cel	11 hybrid.";
7	Genomics 10:214-218(1993).	
RN	[2]	
¥ ;	FUNCTION.	
X 6	MEDLINE V4.Z2.Z0Z0; FUDMGQ BGI/I3Z3;	0 0000000000000000000000000000000000000
£ 6	phronfole B proming I I. Din W & Goodwin B	C.F., Inconton C.,
K E	"A lumabatowin bata anaoritia roccator ".	A.G., SILLLI C.A.,
KI.	*A lymphotoxin*beta*speciiic receptor.";	
٦ ر	SCHEICE ZO4:/U-/10/11994/.	NT NOTTONIA TIMESON
, כ		. FOSSIBLE FUNCTION IN
2 6		Ç
י ני	-!- Subcerrolak Location: Type I membrane process	10.
ខ្ល	-! - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.	
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ייט	This SWISS-PROT entry is copyright. It is produced through a collaboratio	ced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics	and the EMBL outstation
ر ا	the European Bioinformatics institute. There are no restrictions on	re no restrictions on its
ပ္ပ	use by non-profit institutions as long as it	as its content is in no way
ייי	modified and this statement is not removed. Usa	age by and lor commercia
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ပ္ပ	or send an email to license@isb-sib.cn).	
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DR G	EMBL; L04270; AAA36757.1;	
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DR	MIM; 600979;	
DR	InterPro; IPR001368; INFR_c6.	
DR	Pfam; PF00020; TNFR_c6; 4.	
DR	ProDom; PD000771; TNFR_c6; 1.	
DR		
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.	
DR	3.	
ΚW	protein; Repeat;	Signal.
FT	L 30	
FT	435	ECEPTOR.
FT	31 227	ENTIAL).
FT	TRANSMEM 228 248 POTENTIAL.	

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BY
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SIGNAL
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TWER-CYS 1.
TWER-CYS 2.
TWER-CYS 3.
TWER-CYS 4.
  SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%; Score 771; DB 1; 70.7%; Pred. No. 6.7e-59; ive 14; Mismatches 40;
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01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                       MGD; MGI:104875; Ltbr.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
Probom; PD000771; TNFR_c6; 1.
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Best Local Similarity 70.7%
Matches 135; Conservative
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415 AA;
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"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENS 60
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                TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 4.

BY SIMILARITY.

BY SIMI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-96163885; Pubmed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CVB; TISSUE-Lung; MEDLINE-96072804; PubMed-7594541; Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%; Score 1133; DB 1; Best Local Similarity 100.0%; Pred. No. 9.4e-90; Matches 197; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
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LTBR OR TNFCR OR TNFRSF3.
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                                                                                                                                                                                                                                                                                                                                                                                   46709 MW;
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Best Local Similarity
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P50284;
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CARBOHYD
SEQUENCE
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TNR3_MOUSE
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REPUBLICATION OF THE PROPERTY AND DESCRIPTION OF THE PROPERTY 
01-AUG-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor
binding protein 2) (IPPII) (P80) (TNF-R2) (P75) (CD120B) (Etanercept).
TNFRSFIB OR TNFR2 OR TNFR2
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90260639; PubMed=2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE-93016040; PubMed-132824;
MEDLINE-03016040; PubMed-132824;
Medenica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goedel D.V.;
"Biochemical properties of the 75-kDa tumor necrosis factor receptor.
Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 27-31.
MEDLINE-90110215; PubMed=2153136;
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
MEDLINE-91056048; PubMed-2173696;
Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99221490; PubMed-10206649;
Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
"Structural basis for self-association and receptor recognition of
human TRAF2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.", Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).
                                                                                                                                      Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96299745; PubMed=8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91045991; PubMed=2172983;
Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
"A second tumor necrosis factor receptor gene product can shed
naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
Ringold G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 267:21172-21178(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990).
                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brodeur G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brockhaus M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                         Nature 398:533-538(1999).

-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
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TNFR-CYS 2.
TNFR-CYS 3.
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EMBL, U521817, AAC50622.1; JOINED.
EMBL, U52189, AAC50622.1; JOINED.
EMBL, U52189, AAC50622.1; JOINED.
EMBL, U5216, AAC50622.1; JOINED.
EMBL, U52161, AAC50622.1; JOINED.
EMBL, U52161, AAC50622.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U52163; AAC50622.1; JOINED.
EMBL; U52164; AAC50622.1; JOINED.
EMBL; M55994; AAA36755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 4.
                                                                                                   LEVEL ON THREONINE RESIDUES.
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SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M32315; AAA59929.1; -. EMBL; M35857; AAA63262.1; -. EMBL; U52165; AAC50622.1; -.
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PIR, A36007; A36007.
PIR, A36475; A36475.
PIR; B35010; B35010.
PIR; A23666; A23666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1CA9; 12-APR-99.
MIM; 191191; -.
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                                                                                                                                                                    HWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119
                                                                                                                                                                                   86 IMNWVPECLSCGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
                                                                                                                                                                                                               DCPPG----TEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                            Gaps
                                                                                                                          5 AVPPYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                      28 AFIPYAPEPGSICR--LREYIDQIAQMCCSKCSPGQHAKVFCIKISDIVCDSCEDSIYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A., Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";

Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  . .) (POTENTIAL)
                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILMS=91187885; PubMed=1849278;
MEDILMS M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
"Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is species
specific.";
                                                                             26.9%; Score 305; DB 1; Length 461; 35.0%; Pred. No. 4.1e-19;
                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
receptor 2 precursor (TNF-R2) (p75).
                                                                                                    78; Indels
N-LINKED (GLCNAC. .) (POT
R -> P (IN REF. 4).
R -> M (IN REF. 4).
A -> T (IN REF. 4).
A -> T (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kissonerghis M., Fellowes R., Feldmann'M., Chernajovsky Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type I membrane protein -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                                                                                                       474 AA.
                                                                                                   24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91246168; PubMed=1645445;
                                                                                                                                                                                                                                                                                                                          TRIB_MOUSE STANDARD; E
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Last sequ
DT 16-OCT-2001 (Rel. 40, Last anno
                                             WW.
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                                                                                                                                                                                                                                                                                GNASRDAVCTSTSPTRSMAP 211
                                                                                                                                                                                                                                                                                                                                                                                            Tumor necrosis factor recept
TNFRSF1B OR TNFR2 OR TNFR-2
                                   363
48316
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                                                                                                    Conservative
 193
141
196
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 193
141
196
363
461 AA;
                                                                                        Best Local Similarity
Matches 70; Conserv
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 CARBOHYD
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 QFRTCLSCSSSCTTDQV----EIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 PYASE-NQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 474;
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                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.0%; Score 295; DB 1, 34.0%; Pred. No. 3e-18; ive 24; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   625 AA.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                      EMBL; M60469; AAA39752.1; -.
EMBL; M5978; AAA40463.1; -.
EMBL; U39488; AAA85021.1; -.
EMBL; X89128; CAA60618.1; -.
PIR; B38634; B38634.
HSSP; P19438; INCF.
MGD; MGI:1314883; INCF.
INCEPTO; IPRO01368; TNFR_C6; Pfam; PF00020; TNFR_C6; 1.
PCODOM; PD000771; TNFR_C6; 1.
PCAGITE; SWOC28; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
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16-0CT-2001 (
01-MAR-2002 (
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ID TR11_MC
AC 035305;
DT 16-OCT-
DT 16-OCT-
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66621 MW; F8C1872E99511D8E CRC64;

625 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
rumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (ODFR).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                     TISSUE-Fetal liver;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Transmembrane; Repeat; Signal.

1 30 POTENTIAL.
31 625 TUMOR NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99097247; PubMed=9878548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF019046; AAB86810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1314891; Thfrsflla.
InterPro; IPR001368; TNFR_c6.
Pfam. PF00020; TNFR_c6; 3.
ProDom; PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR, 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234
625
69
1113
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1152
61
61
63
63
1128
1128
1128
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1152
                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P25942; 1CDF
                                                              TNFRSF11A OR RANK.
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                               Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
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RAPA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Bailey J., Barlow K.F., Bades K.N., Bearde D.M.,
Bailey J., Barlow K.F., Bates K.N., Berdene D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Elington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Howden P.J.,
RA M. R., Hunt A.R., Hunt S.E., Jeksech K., Johnson D.,
RA M. Kamberley A.M., King A., Krights A., Laird G.K., Lawlor S.,
Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA MINE S., Mistry D., Moore M.J., McConnachle L.J., McConnachle L.J., McConnachle L.J., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams L., Willingy D.R.,
Ra Williang L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                 124 GTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                       64 HWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPP 123
                                                                                Gaps
                                                                                                                                                 4 QAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                              30 QVTPPCTQE-----RHYBHLGR-CCSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Last sequence update)
01-MAK-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89356608; PubMed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
A.B.lymphocyte activation molecule related to the nerve g factor receptor and induced by cytokines in carcinomas.";
EMBO J. 8:1403-1410(1989).
                                                                            85; Indels
   DB 1;
Score 283; DB 1
Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 AA
                                                                        25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last seq
01-MAR-2002 (Rel. 41, Last ann
25.0%;
32.6%;
                                                                            Conservative
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                                          Sest Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 KNPL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 SSSM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNR5_HUMAN P25942;
                                                                            90;
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNR5_HUMAN
                                                                        Matches
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67 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTE 126

δ

22 PPTA----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWN 72

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                                                                                                                               A Description of CD40L

RA Singh J., Garber E., van Vijimen H., Karpsusas M., Hsu Y.-M.,

RA Singh J., Garber E., van Vijimen H., Karpsusas M., Hsu Y.-M.,

RA Zheng Z., Naismith J.H., Thomas D.;

RT The role of polar interactions in the molecular recognition of CD40L

RT with its receptor CD40.";

Protein Sci. 7:1124-1135(1998).

C. -- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

C. -- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND FROWN.

C. -- STMLEAR LOCAPION: Type I membrane protein.

C. -- SIMLEARTY: CONTAINS 4 TWFR-CYS REPEATS.

C. -- STMLEARTY: CONTAINS 4 TWFR-CYS REPEATS.

C. -- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;

WWW-"http://www.ncbi.nlm.nh.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                       οŧ
                                                                  "Construction and analysis of a detailed three-dimensional model the ligand binding domain of the human B cell receptor CD40."; Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
Probom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR_AG:
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                   [4]
3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                          MEDLINE=97189482; PubMed=9037712;
                            3D-STRUCTURE MODELING OF 24-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL035662; CAC17670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30619 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X60592; CAA43045.1; -.
Nature 414:865-871(2001).
                                                        Bajorath J., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S04460; S04460.
PDB; 1CDF; 01-APR-97.
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83
105
111
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194
216
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104
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familial expansile osteolysis.";

Nat. Genet. 24:45-48(2000)

-!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS

OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-
MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
INTERACTIONS BETWEEN T-CELLS AND DENDRATIC CELLS.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Fotential).
-!- TISSUE SPECIFICITY: UBLOUITOUS EXPRESSION WITH HIGH LEVELS IN
SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLAND.

GLAND.

JESASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE OSTEGASE: DEFECTS (FEQ), A RARE AUTOSOMAL DOMINANT BONE DISORDER CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE STEDARCTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING THE ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFHESS AND LOSS OF DENTITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET DISEASE DE BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDBZ). IT AS A BONE REMODELLING DISCADER WHITH CLINICAL SIMILARITIES TO FEO. UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galibert L.;
"A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
Nature 390:175-179(1997).
Υ.
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                                                                                    127 AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano Morinaga T., Higashio K.;
Morinaga T., Higashio K.;
MRANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis.";
Biochem. Biophys. Res. Commun. 253:395-400(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (Osteoclast differentiation factor TNFRSF11A, OR RÄNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson D.M.; "Mutations in TNFRSF11A, affecting the signal peptide of RANK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Dendritic cell;
MEDLINE-98012977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H., Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
                                                                                                                                                                                                        616 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20082806; PubMed=10615125;
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                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                          TR11_HUMAN
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Gaps

12;

24.5%; Score 278; DB 1; Length 277; 35.0%; Pred. No. 5.2e-17; ive 20; Mismatches 83; Indels

Conservative

62;

Matches

Similarity

Query Match

Best Local

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HSSP; P25942;
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DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
REPEAT
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REPEAT
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RESULT 8
TNR5_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNE 63
                                                                                                                                                                                  Receptor; Glycoprotein; Transmembrane; Repeat; Signal; Polymorphism;
Disease mutation.
                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
ALLLLCALL -> ALLLLCALLLCALL (IN
                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                             LLCALL -> LLCALLLLCALL (IN FEO).
                                                                                                                                                                                                          TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.4%; Score 277; DB 1; Length 616
31.7%; Pred. No. 1.3e-16;
ive 28; Mismatches 87; Indels
                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      'FTId=VAR_011518.
E3DE9A7A08196F81 CRC64;
                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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                                                                                                                                                                                                                                                    TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                   EMBL; AF018253; AAB86809.1; -. HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                            InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              616 AA; 66033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 31.7 Matches 60; Conservative
                                                                                                                                                       SMART; SM00208; TNFR; 4.
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                                                                                                   MIM; 603499;
MIM; 174810;
MIM; 602080;
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                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminanția; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97281252; PubMed-9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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PROSITE; PS50050; TUFR_NGFR_2; 1.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19 POTENTIAL.
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                                                                                                                                member 5 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunology 90:294-300(1997).
--- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
--- SUBCELLULA: TOCATION: Type I membrane protein.
--- SIMILARITY: CONTAINS 4 INFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                            (CD40L receptor) (B-cell surface antigen CD40) (Fragment) INFRSF5 OR CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
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                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily men
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TNER-CYS 3.
TNER-CYS 4.
BY SIMILARITY.
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TNR5_BOVIN STANDARD; 028203; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequinov-12001 (Rel. 40, Last annover-2001 (Rel. 40, Last annover-2001)
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ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
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SEQUENCE FROM N.A.
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                                                  86 NLGLRIQSEGTLNTDTICVCVEGQHCTSHT--CESCTPHSLCLPGFGVK---QIATGLLD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
                                  80 VMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKG--N 137
            85
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-92105763; PubMed-1370315;
Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";
J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00208; TNFR; 4. PROSTE; PS00562; TNFR, MGFR_1; 1. PROSTE; PS00562; TNFR_MGFR_1; 1. PROSTEE; PS50050; TNFR_MGFR_2; 4. Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=Liver;
STRAIN-BALB/C; TISSUE=Liver;
MEDLINE-93094586; Pubmed=1281194;
Grimmldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Torres R.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                138 NHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                   289 AA
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                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001368; TNFR_c6. Pfam; PF00020; TNFR_c6; 4. ProDom; PD000771; TNFR_c6; 1.
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                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                    INFRSF5 OR CD40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97306336; PubMed-9162061; Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J., Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C., Wang S., Gentz R., Yu G.-L., Young P.R.; "A newly identified member of the tumor necrosis factor receptor superfamily with a wide tissue distribution and involvement in Jymphocyte activation."

J. Biol. Chem. 272:14272-14276(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-cervical adenocarcinoma;
MEDILINE-97053782; PubMed-8898196;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
Merpes simplex virus-1 entry into cells mediated by a novel member the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG----TEAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Herpesvirus entry mediator) (Tumor necrosis factor receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor necrosis factor receptor superfamily member 14 precursor
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                       EXTRACELLULAR (POTENTIAL).
                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                    SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                            21.5%; Score 243.5; DB 1
31.0%; Pred. No. 4.7e-14;
ive 22; Mismatches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TR14_HUMAN STANDARD; PRT; 283 AA. 092955; 09UM65; 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update) 16-007-2001 (Rel. 40, Last annotation update)
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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289 AA;
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271 AA

PRT;

STANDARD;

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165 --- CPP 167
                                              TNR4_RAT
P15725;
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
      SUBCELULAR LOCATION: Type I membrane protein (Probable).
TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION IN LUNG, SPLEEN, AND THYMUS.
SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAPGTAQSDTTCKNP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 PPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 283;
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                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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46CE13C2C70242C1 CRC64;
                                                                                                                                                                                                                                                                                  Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFC----
                                                                                                                                                                                                                                                                                                              SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.3%; Score 230.5; DB 1
30.1%; Pred. No. 5.9e-13;
iive 13; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                          InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                               EMBL, U70321; AAB58354.1; -. EMBL, U81232; AAD00505.1; -. EMBL, AF153978; AAF75588.1; -. HSSP; P25942; 1CDF.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   MIM; 602746
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TRANSMEM
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                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 MGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHC 140
            01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                Mallett S., Fossum S., Barclay A.N.; "Characterization of the MRC OX40 antigen of activated CD4 positive 1 lymphocytes -- a molecule related to nerve growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 KEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 KDIYPSGHK-CCRECQPGHGMVSRCDHTRDIVCHPCEPGFYNEAVNYDT-CKQCTQCNHR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00652; TNRR_NGFR_1; 3.
PROSITE; PS00652; TNRR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat; Signal.

1 19 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINKED (GLCNAC. . .) (POTENTIAL) C06465136B16E821 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
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                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 9:1063-1068(1990).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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TNFR-CYS 4.
N-LINKED (GI
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TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                            MEDLINE=90214614; PubMed=2157591;
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PIR; S08036; S08036.
PIR; S12783; S12783.
HSSP; P19438; 1EXT.
InterPro; IPR001368; TNFR_C6.
Pfam; PP00020; TNFR_C6.
ProDom; PD000771; TNFR_C6.
SMART; SM00208; TNFR: 3.
  (Rel. 14, Created)
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271 AA;
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                                                                                                                                                                                                               NCBI_TaxID=10116;
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01-APR-1990
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                  ----PGTQPR-QDSSHKLGVDC 122
                                                                                                                                                                                                                                                    (Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
sis factor receptor superfamily member 4 precursor (0X40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE 94044750; PubMed=8228223; Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J., Claassen E., Noelle R.J., Fell H.; "Cloning of mouse 0x40: a T cell activation marker that may mediate T.B cell interactions."; Immunol. 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene structure and chromosomal localization of the mouse homologue
                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-95255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                        141 VPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
                                                                              CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3 (INCOMPLETE).
TNER-CYS 4.
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EMBL; X85214; CAA59476.1; --
HSSP; P19438; 1ExT.
MGD; MGI:104512; Trirsf4.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
ProDom; PD000771; TNFR_C6; 1.
                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
receptor) (OX40 antigen). TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
103
124
165
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Eur. J. Immunol. 25:9
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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212
237
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                                                                                                                                                                                                                                                      01-FEB-1996
16-OCT-2001
                                                                                                                                                                                              TNR4_MOUSE
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TRANSMEM
DOMAIN
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MEDLINE=90235285; PubMed=2158863; Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.; Molecular cloning and expression of a receptor for human tumor necrosis factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201. MEDLINE=91006021; PubMed=1698610; Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Aderka D., Holtmann H., Wallach D.; Soluble forms of tumor necrosis factor receptors (TNF-Rs). The CDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
MEDLINE=91090841; PubMed=1702293;
MEDLINE=91090841; PubMed=1702293;
MEDLINE=91090841; PubMed=1702293;
MEDLINE=9.
Manter-Popy I., Kroenke M., Scheurich P., Pfizenmaier K.,
Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
"Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein.";
DNA Cell Biol. 9:705-715(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 KHTYPSGHK-CCRECQPGHGMVSRCDHTRDTLCHPCETGFYNEAVNYDT-CKQCTQCNHR
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01-FEB-1991 (Rel. 17, Last sequence update)
11-COT-2001 (Rel. 40, Last annotation update)
11-FEB-101 (Rel. 17, Last annot
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                    Length 272;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 VPCKAGHFONTSSP--SARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
N-LINKED (GLCNAC. . .) (Pa
A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                         ch 18.9%; Score 214.5; DB 1
1 Similarity 31.7%; Pred. No. 1.3e-11;
53; Conservative 16; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 AA
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     144 N
15 A
30153 MW;
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                                                                                                            272 AA;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TR1A_HUMAN
     CARBOHYD
CONFLICT
SEQUENCE
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TR1A_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structure 4:1251-1262(1996).

-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECEPTOR: THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSCOURT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYTOCIDAL THE BEFREGIS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPHINGOMYELINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBDIVIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERI LEADS TO MOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERFACE SPECIFICALLY WITH THE DEATH DOMAIN OF TRAND. VARIOUS TRAND-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FAND, ARE RECRUITED TO TRAIL OWNELEX BY THEIR ASSOCIATION WITH TRAND. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB MEDLINE-93258809; PubMed=8387891;
                                                                                                                                                                                                                                              SEQUENCE OF 41-45.
MEDLINE-9010215; PubMed-2153136;
MEDLINE-9010215; PubMed-2153136;
Brgelmann H., Novick D., Wallach D.;
Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface urine.
                                                                                                                                                                                                                                                                                                                                                                                                      Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
Broger C., Loetscher H., Lesslauer W.;
"Crystal structure of the soluble human 55 kd TNF receptor-human TNF
beta complex: implications for TNF receptor activation.";
Cell 73:431-445(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
MEDINTE-97049483, PubMed-8939750,
Malsmith J.H., Devine T.Q., Khono H., Sprang S.R.;
"Structures of the extracellular domain of the type I tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLUIAR LOCATION: Type I membrane protein.

DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL.

THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH

NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

SIMILARITY: CONTAINS 1 DEATH DOMAIN.

SIMILARITY: CONTAINS 1 DEATH DOMAIN.

BATABASE: NAME-PROW: NOTE-CD guide CD120a entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
                                                                    and
                                                                                                                                             MEDLINE-92250049; PubMed-1315717;
Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
"Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
localization to chromosome 12p13.";
Genomics 13:219-224(1992).
                                                Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.; "Cloning of human tumor necrosis factor (TINF) receptor CDNA expression of recombinant soluble TNF-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
                                                                                                                                                                                                                                                                                                                           nor necrosis factor receptors.";
Biol. Chem. 265:1531-1536(1990).
SEQUENCE FROM N.A.
TISSUE-Placenta;
MEDLINE-91017509; PubMed-2170974;
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                                                                                                                                  SEQUENCE FROM N.A.
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EMBL;
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TUMOR NECROSIS FACTOR RECEPTOR 1.
TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 DREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENH 95
                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> T (IN DBSNP:1804532).
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DEATH.
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MISSING (IN REF. 4).
GPAA -> APP (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.6%; Score 210.5; DB 32.6%; Pred. No. 4.6e-11 iive 19; Mismatches 8
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
", M63121; AAA36754.1; -.
", M78866; AAA61201.1; -.
", M78864; AAA61201.1; JOINED.
", M78865; AAA61201.1; JOINED.
", M60275; AAA36756.1; -.
", A21522; CAA01558.1; -.
                                                                                                                                                                                                                                                                            PROSITE: PS00652; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 3. PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                           Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
Probom; PD000711; TNFR_c6; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00006; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50494 MW;
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InterPro; IPR001368; TNFR_c6.
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166
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191
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1NCF; 07-DEC-95.
1EXT; 11-JAN-97.
                                                                                A34899; GQHUT1.
A35010; A35010.
                                                                                                         S12057.
A38208.
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455 AA;
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CARBOHYD
CARBOHYD
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                                                        EMBL;
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TR1A_PIG
P50555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.; "Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LTICQLCR-PCDPVMGLEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 PYTPPNGKCKDIEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPGGSGTFTSRNNH 79
                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                 protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-1- SIMILARITY: CONTAINS 2 TWFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210; DB 1; Length 349;
Pred. No. 4e-11;
); Mismatches 80; Indels
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TNFR-CYS 2.
D45D40B5C6E780EF CRC64;
                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
101-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Protein C22/B28 homolog.
                                                                                                                                             349 AA.
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                                                                                                                                             PRT;
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MEDLINE-93202281; PubMed-8384129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 2.
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108 TNI
38189 MW; 1
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InterPro; IPRO01368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
ProcDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
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EMBL; X67117; CAA47540.1; --
PIR; D36858; D36858.
PIR; S35987; S35987.
PIR; S46888; S46888.
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67
349 AA;
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Best Local Similarity
Matches 45; Conserv
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NCBI_TaxID=10255;
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                                         181 TTCKNPL 187
                                                                    210 TTVLLPL 216
                                                                                                                                                                                                                                             Variola virus.
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                                                                                                                                                                                                                                                             Suter B., Pauli U.H.;

"Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
receptor.";

Gene 163:263-266(1995).

-I- FINCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
GEGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
RECRUITS CASPASE-8 PROTECLIVIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPATARE-SPECIFIC CYSTEINE
RECRUITS THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERI LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD. INTERACTING
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERACTING
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NP. KAPPA B SIGNALING (BY SIMILARITY).

-I- SUBCLILULAR LOCATION: TYPE I membrane protein.

-I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RI)
                                                                                                                                                  Chordata; Craniata; Vertebrata: Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
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TUFR-CYS 2.

TUFR-CYS 3.

TUFR-CYS 4.

N-SMASE ACTIVATION DOMAIN (NSD).

DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. CYTOPLASMIC (POTENTIAL).
 461 AA
PRT;
                                                                                                                                                                                                                                                 MEDLINE=96011645; PubMed=7590278;
                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P19438; 1TNR.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U19994; AAC48499.1; -.
 STANDARD;
                                (Rel. 34, C
(Rel. 34, I
(Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
210
210
210
2233
461
125
1166
1195
447
                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                 TNFRSF1A OR TNFR1.
                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                TISSUE=Kidney;
                                01-0CT-1996
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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us-09-299-139a-1\_1.rsp

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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 LTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWA---LECTHCELLSDCPPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.2%; Score 206; DB 1; Length 461;
Best Local Similarity 29.4%; Pred. No. 1.1e-10;
Matches 57; Conservative 22; Mismatches 77; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |-|| :| || :| ||-|| :| ||-|| :| ||-|| :| ||-|| :| ||-|| :| ||-|| :| ||-|| :| ||-|| :| ||-|| 36 DREKRESLCPQGKXSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENH 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 DQEK------EYYEPQHR-ICCSRCPPGTYVSAKC-SRIRDIVCATCAENSYNEHWNY 67
BY SIMILARITY.
BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 NDFODTGTTVLLPL 215
    DISULFID
CARBOHYD
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Search completed: October 4, 2002, 10:15:23 Job time: 241 sec

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us-09-299-139a-1\_1.rspt

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October 4, 2002, 10:11:47; Search time 26.58 Seconds (without alignments) 1282.167 Million cell updates/sec
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1133
1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNFLEPLPPEMSGT 197
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
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1: Sp_acrhea:*
2: Sp_bacteria:*
3: Sp_lougi:*
4: Sp_louna:*
5: Sp_louna:*
5: Sp_mammal:*
5: Sp_nortebrate:*
5: Sp_organelle:*
5: Sp_organelle:*
5: Sp_louna:*
5: Sp_louna:*
5: Sp_organelle:*
5: Sp
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

## SUMMARIES

		Description	016042 homo sapien	091zm6 rattus norv	062327 mus musculu	095407 homo sapien	O88734 mus musculu	O9byu0 homo sapien	O99ne0 musculu	O99nel mus musculu	O99ne2 mus musculu	Q9xsz8 cercopithec	008712 mus musculu	072735 cowpox viru	Oguhp4 homo sapien	000300 homo sapien	O9pusO salvelinus	008727 rattus norv
		ΙD	016042	Q912M6	062327	095407	088734	Q9BYU0	Q99NE0	099NE1	099NE2	09xSz8	008712	072735	Q9UHP4	000300	OSD460	008727
		DB	4	11	11	4	11	4	11	11	11	9	11	12	4	4	13	11
		Match Length DB	425	433	459	300	482	203	260	222	234	283	401	186	372	401	302	401
æ	Query	Match	25.7	25.7	25.6	25.3	24.4	22.3	22.2	21.5	21.5	21.4	21.4	21.2	21.1	21.1	21.0	20.8
		Score	291.5	291.5	290	285.5	276.5	252.5	251.5	243.5	243.5	242.5	242.5	240	239.5	239.5	238	235.5
	Result	No.	П	2	m	4	S	9	7	80	σ	10	11	12	13	14	15	16

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15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWYLTICQLC 74 | | | :| | :| | :| | | | | | | |

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Q96131 homo sapien Q9dd2 gallus gall Q9dd2 gallus gall Q9dw71 oncorbynchu Q90w71 oncorbynchu Q9bw71 oncorbynchu Q91w77 mus musculu Q91w77 mus musculu Q91sm6 gallus gall Q998 camelpox viru G57098 camelpox vi G57099 camelpox vi G57099 camelpox vi G57099 camelpox vi G57099 camelpox vi G57109 monkeypox v Q911r5 vaccinia vi G57100 monkeypox v G57110 monkeypox v	O57101 monkeypox v
e Marie III.	
4 Q96J31 13 Q9DDD2 12 Q57117 3 Q90W71 14 Q9EPU5 11 Q91W77 12 Q97 P87 12 Q97 P87 12 Q97 P87 12 Q97 Q97 12 Q97 Q97 Q97 12 Q97 Q97 Q97 12 Q97 Q97 Q97 Q97 12 Q97	
22 28 28 28 28 28 28 28 28 28 28 28 28 2	349
230.5 230.5 230.5 230.2 230.2 228.5 238.5 23	19.1
1199 1199 1199 1199 1199 1199 1199 119	45

## ALIGNMENTS

	<pre>: Buteleostom1; e: Homo. H.W., Gentz R., c, but distinct</pre>	564;	Length 425; Indels 27; Gaps
PRELIMINARY; PRT; 425 AA. (TrEMBLrel. 01, Created) (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation update); IS FACTOR RECEPTOR (FRAGMENT).	Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;  NCBI_TaxID=9606;  SEQUENCE.FROM N.A.  MEDLINE=91370690; Pubmed=1966549;  Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,  Brockhaus M., Lesslauer W.;  "Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences."	1. 3. 1B24A97E3AD4CF9F CRC64;	Score 291.5; DB 4; Pred. No. 1.8e-23; 24; Mismatches 73;
2 2016042 PRELIMINARY; PRT; 425 A 016042; Ol-NOV-1996 (TEMBLE). 01, Created) 01-JUN-2001 (TEMBLE). 17, Last sequence 01-JUN-2001 (TEMBLE). 17, Last annotatio TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).	Homo saplens (Human). Eukaryota; Metazoa; Chordata; Cran Mammalia; Eutheria; Primates; Cata NCBL_TaxID=9606; SEQUENCE.FROM N.A. MEDLINE-91370690; Pubmed=1966549; Dembic Z., Loetscher H., Gubler U. Brockhaus M., Lesslauer W.; Thyo human TNF receptors have simi	(1990). 9824.2; 98; TNFR_C6. TNFR_C6; 1. TNFR_C6; 1. TNFR_NGFR_1; 1. TNFR_NGFR_2; 3.	25.7%; 34.4%; vative 24
1 2 2 2 216042 PRELIN 01-809-1996 (TrEM) 01-100-2001 (TrEM) 01-JUN-2001 (TrEM) 01-JUN-2001 (TrEM) TUMOR NECROSIS FAC	Homo sapiens (Human). Eukaryota; Metazoa; Chordata Mammalia; Eutheria; Primates NCBL_TaxID=9606; SEQUENCE.FROM N.A. MEDLINE-91370690; PubMed=196 Dembic Z., Loetscher H., Guk Brockhaus M., Lesslauer W.; "Two human TNF receptors hav	Cytokine 2:231-237(1990).  EMBL: \$63368; AAB19824.2; -  HASPP: \$25942; 1CDF.  InterPro; IPR001368; TNFR_C6; 1.  PRODON TO THER_C6; 1.  PROSITE; PS00652; TNFR_NGFR_1;  PROSITE; PS50050; TNFR_NGFR_1;  PROSITE; PS50050; TNFR_NGFR_2;  PROGENCE 425 AA; 44608 MW;	Simi 5;
SUL 604	OS HOM OC MAM OC MAM OC MCB OX NCB RN [1] RA MED RA DEM RA Bro RT int		Query Match Best Local Matches 6

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PRELIMINARY;
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87
93
268
345
421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 VC----APESPTLS 195
                                                                                   [2]
SEQUENCE FROM N.A.
                                                                         Genomics 0:0-0(0).
                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                    Receptor.
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VARIANT
VARIANT
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VARIANT
VARIANT
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                            126 EAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEÅAPGTAQSDTTC-- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 LTICOLC-RPC--DPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDCP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 LHTCLSCSSSCSDDQV----ETHNCTKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                       Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                    8 PYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSC
                  75 R---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLSDCPPG----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                          25.7%; Score 291.5; DB 11; Length 433; 33.3%; Pred. No. 1.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MURINE TUMOUR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                     433
45723 MW; 75736D835E72CA4A CRC64;
                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                                                                           433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 AA.
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                                                                                                                                                                            Created)
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                   Q91ZM6;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CKNPLEPLPPEMSGT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASE-SPIPSAVPRI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                              433 AA;
                                                                                          184 KNPLEPLPP 192
                                                                                                           167 TSPTRSMAP 175
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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SEQUENCE
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Q62327;
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Matches
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Q912M6
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Q62327
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67 YLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCELLSDC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 PPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095407;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DECY RECEPTOR 3 (M68 ) (M68C) (M68E) (DJS83P15.1.1) (TUMOR NECROS)
DCR3 OR TRE OR TNFRSF6B.
DCR3 OR TRE OR TNFRSF6B.
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            is
                                                                                                                                                                                                                                                                                                               Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                                          ~
                                                                                                                                Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
"Amino acid variation in the tumor Nerrosis factor receptor
linked to autoimmune diabetes in NOD mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> I.
-> F.
-> C.
6C51D2CF1C4626DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>^</u> ^
                                                                                                                                                                                                                                                                        STRAIN=NOD;
MEDLINE=95178848; PubMed=7873884;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001368; TWR_c6.
Pfam: PF00020; TWFR_c6; 4.
ProDom; PD000771; TWFR_c6; 1.
SMART; SM0208; TWFR, NGFR_1; 2.
PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 3.
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MEDLINE-99087326; PubMed-9872321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48686 MW;
                                                                                                                                                                                                                                                                                                                                                                               Mamm. Genome 5:726-727(1994).
EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
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Matches 65; Conservative
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482 AA.

PRT;

PRELIMINARY;

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Receptor.
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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Grineng A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.; "Genomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-2012600; PubMed-10655113; MEDLINE-20125600; PubMed-10655113; MEDLINE-20125600; MEDLINE-20125600; MEZKER M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%; Score 285.5; DB 4; Length 300; 36.0%; Pred. No. 5.7e-23; Indels 17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN----PLEPLPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99253915; PubMed-10318773; Yu K.Y. Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.; "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis."; J. Biol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
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TISSUE=LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
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ProDom; PD000771; TNFR_c6; 1.
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                                                                            Nature 396:699-703(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (NOV-2001)
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Best Local Similarity
Matches 63; Conserv
                                                                                                        SEQUENCE FROM N.A.
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                                                                   colon cancer
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SEQUENCE
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RESULT 088734

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MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

MEDLINE-98414512; PubMed-9740674;

The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
and Characterization of the two Transcripts.";

Genomics 22:79-98(1980).

EMBL; Y14619; CAA74969.1; JOINED.

EMBL; Y14621; CAA74969.1; JOINED.

REMBL; Y14622; CAA74969.1; JOINED.

REMBL; Y14622; CAA74969.1; JOINED.

REMBL; Y14679; CAA74969.1; JOINED.

REMBL; Y14679, CAA74969.1; JOINED.

REMBL; Y14679, CAA74969.1; JOINED.

REMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 SYNEHWNYLTICQLCR---PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA--AWALECTH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
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SEQUENCE FROM N.A.
MEDLINE=21117110; PubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 AA; 51106 MW; F6C15046B48FF83C CRC64;
                                       Last sequence update)
Last annotation update)
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Last annotation update)
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       Created)
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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08,
19,
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                                       (TrEMBLrel.
   (TrEMBLrel.
                                                                        01-DEC-2001 (TrEMBLrel
P80 TNF-ALPHA RECEPTOR
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                                                                                                                                                                             Mus musculus (Mouse)
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Best Local Simi
Matches 65;
01-NOV-1998
01-NOV-1998
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Best Local Similarity 31.7% Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENGGLVEAAPGTAQS----- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 PPTA-----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWN 72
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REGULARIATION OF CD40 function by its isoforms generated through a iternative splicing.";

RT TONE M. TONE Y. Waldmann H.;

REGULARIATION OF CD40 function by its isoforms generated through a iternative splicing.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

EMBL; AJ401390; CAC29430.1; -.

BR PSP; P25241; LCFE

DR HSPS; P25242; LCFE

DR InterPro; IPR001005; Ribosomal_S2.

InterPro; IPR001065; Ribosomal_S2.

DR Pfam; PF00007; TNFR_C6; 1.

DR Prodom; PD000771; TNFR_C6; 1.

DR PROSITE; PS00037; MTPL]; UNKNOWN_1.

DR PROSITE; PS000652; RIBCSOMAL_S2.1; UNKNOWN_1.

DR PROSITE; PS000652; TNFR_NGFR_1; 1.

DR PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.

PROSITE; PS000652; TNFR_NGFR_1; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
*Regulation of CD40 function by its isoforms generated through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.3%; Score 252.5; DB 4; Length 203; Best Local Similarity 33.2%; Pred. No. 1.5e-19; Matches 63; Conservative 21; Mismatches 75; Indels 31.
                                                                                                                                                InterPro; IPR000561; EGF-11ke.
InterPro; IPR000561; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
Proport; PM00208; TNFR_c6; 1.
SMART; SM00208; TNFR, 4.
PROSITE; PS00050; TNFR, 1.
PROSITE; PS00050; TNFR_NGFR_2; 3.
SEQUENCE 203 AA; 22259 MW; 0739905F79059A4F CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CD40 TYPE V ISOFORM.
                                 aiternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001)..
EMBL; AJ300189; CAC29424.1; -.
HSSP; P25942; LCDF.
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181 LRDPVC-HPL 189
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Q99NE0;
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                                                                                                                                              75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
                                                                                                                                                                        130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC----KN 185
                                                                                                                                                                                                                                                      139 TDTV-----CHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVICEKVVKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG----TEAEL 129
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 74
                                                              15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC
                                                                                      25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDIV-----CHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 222;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EE21E6C76FB42DEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
31.7%; Pred. No. 2.4e-19; ive 22; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.5%; Score 243.5; DB 1.31.0%; Pred. No. 1.5e-18; iive 22; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEGUIN PRODUCT: THER_G6; 4.

ProDom: PD000771; THER_G6; 1.

SMART; SM00208; THER; 4.

PROSITE: PS00037; NYB_1; UNKNOWN_1.

PROSITE: PS00052; RIBOSOMAL_S2_1; UNKNOWN_1.

PROSITE: PS00062; THRE_NGFR_1; 1.

SEQUENCE 222 AA; 24499 WW; EE21E6C76FB42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TIEMBLEEL 17, CL
01-JUN-2001 (TIEMBLEEL 17, LG
01-DEC-2001 (TIEMBLEEL 19, LG
CD40 TYPE IV ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                186 PL--EPLPP 192
                                                                                                                                                                                                                                                                                                                                                  193 PKDNEMLPP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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DB 11; Length 260;

Score 251.5;

22.28;

Query Match

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Query Match
                                                                                                                                                                                                                                                                              Sest Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              008712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
008712
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
    RL
DR
DR
DR
DR
SQ
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 RPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPG-----TEAEL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHCEPNQGLRVKKEGTAESDTVCTCKEGQHCT--SKDCEACAQHTPCIPGFGVMEMATET 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 TCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQH 80
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecus aethiops (Green monkey) (Grivet).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .17;
                                                                                                                                                                                                                                                                                              MEDLINE=21117110; PubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
"Regulation of CD40 function by its isoforms generated through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00DB1DD38347E325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                           aiternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
EMBL; AJ401388; CAC29428.1; -.
HSSP, P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.5%; Score 243.5; DB 1
31.0%; Pred. No. 1.6e-18;
iive 22; Mismatches 81
                      234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 AA
                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99296730; PubMed=10366573;
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00962; RIBOSOMAL_S2_1;
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00020; INFR_c6.
ProDom; PD000771; INFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00208; TNFR; 4.
E; PS00037; MYB_1; UNKNOWN_1
                                                    .....2001 (TrEMBLrel, 17, C. 01-DEC-2001 (TrEMBLrel, 19, La. CD40 TYPE III ISOFORM. CD40. Mus. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25747 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                      PRELIMINARY;
                                                                                                                                                                     musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09XSZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62SX60
                      099NE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q9XSZ8
099NE2
                        SO DRA RATA A SO DE LA LA COLLA COLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 TICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAW-ALECTHCELLSDCPPGTEA 127
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 YASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 YAPALPSCK--EDEY--PVGSECCPKCGPGFHVRQACGEQTGTVCEPCSPGTYIAHFNGL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ELKDEVGKGNNH-----CVPCKAGHFONTSSPSARCOPHTRCENGGLVEAAPGTAQS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-2091 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
03-ZUD-ROFFGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * STROMAL CELLS AND OSTEOCLAST PROGENITORS.
-1: SUBGUIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
-1: SUBCELLULAR LOCATION: EXTRACELLULAR.
-1: TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
                                                                                                                                                                                                                                                                                                                                                                 21.4%; Score 242.5; DB 6; Length 283; 32.2%; Pred. No. 2.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                      397951C6617FE3AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-KIDNEY;
MEDLINE-97262071; PubMed-9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/OLA, AND NIH SWISS;
MEDLINE=98382527; PubMed=9714833;
                                                                                                                                                                                                           PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 283 AA; 30199 MW;
                                                                                       InterPro; IPR001368; TNFR_c6.
Pfam; PF000020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
Virology 258:365-374(1999).
EMBL; AF147720; AAD37381.1;
HSSP; O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                               57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               008712; 070202;
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A53R PROTEIN.
                            072735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
Q9UHP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UHP4
           12
         RESULT
072735
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BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND PLACEMYA. NOT DEFECTED IN SPLEEN.
-!- DEVELOPMENTAL STRAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 VMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOSVKO--ECNRTHNRVCECEEGRY-----LEIEFCLKHRSCPPGS-GVVQAGTPERNTV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 YYEPQ--HRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRP-CDP 79
                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                             SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                   -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> A (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%; Score 242.5; DB 11; Length 401; 29.6%; Pred. No. 3.4e-18; Ive 25; Mismatches 83; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNRE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAA6102D3B312470 CRC64;
                                                                                                                                                                                                                                               OSTEOPROTEGERIN.
                                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
                                                                                                                                                                                            X TNFR-CYS.
                                                      EMBL, U94331; AAB53708.1; EMBL, AB013898; BAA528269.1; EMBL; AB013893; BAA33388.1; EMBL; AB013899; BAA33388.1; JOINED. EMBL; AB013900; BAA33388.1; JOINED. EMBL; AB013901; BAA33388.1; JOINED. EMBL; AB013902; BAA33388.1; JOINED.
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SWISS)
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                                                                                                                             MGD; MGI:109587; Thirsfilb.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
Probom; PD000771; TNFR_c6; 1.
SMART; SM0005; DEATH; 1.
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                                                                                                                       P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                      15 TO DAY 17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288
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DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                        HSSP;
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63 EHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA---AWALECTHCELLS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYN 62
                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 PTPLPPHAPVNGSC--DEGEYLDKRHNQCCNQCPPGEFAKVRCSGSDNTKCERCPPHTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 AIPNYSNGCHQCRKC-PIGSFDKV-KCIGIQNSKCSCLPGWYCAIDSSQIEDCRDCVPKS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He Z. Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and Expression of Osteoprotegerin from Homo sapiens.";
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
EMBL: AF134187; AAF20168.1;
HSSP: PS5942; ICDF.
InterPro; IPR000488; Death.
InterPro; IPR0001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN-GRI-90; MubMed-9568042; MEDLINE-98229462; PubMed-9568042; Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A., Ryazankina O.I., Gutorov V.V., Kotwal G.J.; Species-specific differences in genome organization of cowpox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.2%; Score 240; DB 12; Length 186; 32.2%; Pred. No. 3e-18; ive 25; Mismatches 66; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D2342F1040A00AE3 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OSTEOPROFEGERIN (FRAGMENT).
                                                      Created)
Last sequence update)
Last annotation update)
186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 RCPCGYFGGIDEQ---GNPICKSCCVGEY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 DCPPGTEAELKDEVGKGNNHCVPCKAGHF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   smallpox, and vaccinia viruses.";
Virology 243:432-460(1998).
EMBL, Y15035, CAA75273.1; -.
HSSP; P25942; LODF.
InterPro; IPR001368; TNFR_C6.
ProDom; PR000020; WTRR_C6; 2.
ProDom; P000071; TNFR_C6; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 186 AA; 20482 MW;
                                                      01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 32.25
Matches 48; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                      Cowpox virus (CPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Orthopoxvirus.
NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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09PUS0
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Q9PUS0
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MEDLINE-97262071; PubMed-9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Lucthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Highes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LUNG FIBROBLAST;
MEDLINE-90151033; PubMed=9492069;
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
Tsuda E., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                                                                                                                                                 84 EEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPC 143
                                                                                                                                                                                                                                                       KQ--ECNRTHNRVCECKEGRY----LEIEFCLKHRSCPPGF-GVVQAGTPERNTVCKRC 124
                                                                                                                                                         Gaps
                                                                                                                                                                                              EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRP-CDPVMGL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-STEOPROTECBRIN PRECINSOR (OSTEOCHASTOGRNESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
                                                                                                                                                         6
                                                                                                                               Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashlo K., "Cloning and characterization of the gene encoding human osteoprortegerin/osteoclastogenesis-inhibitory factor."; Eur. J. Biochem. 254:685-691(1998).
                                                                                                                                                         84; Indels
Pfam; PF00020; TNFR_c6; 3.

Prodom; PD000771; TNFR_c6; 1.

SMART; SM00005; DEATH; 1.

PROSITE; PS00552; TNFR, 4.

PROSITE; PS0059; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS0090; TNFR_NGFR_2; 2.

NON_TER 1 1 1 SEQUENCE 372 AA; 42758 WW; F02527ASCD01CCD3 CRC64;
                                                                                                                                                                                                                                                                                   144 KAGHFONTSSPSARCOPHTRCENOGLVEAAPGTAQSDTTCKNPLE 188
                                                                                                                                                                                                                                                                                                  125 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSE 169
                                                                                                                                DB 4;
                                                                                                                             21.1%; Score 239.5; DB 4
30.9%; Pred. No. 6.8e-18;
iive 21; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                         401 AA.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinology 139:1329-1337(1998),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98351569; PubMed=9688283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoclastogenesis in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFRSF11B OR OPG OR OCIF.
                                                                                                                                                        51; Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human).
                                                                                                                               Query Match
Best Local Similarity
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000300
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FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE, MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERPUTING CELL-FO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENTYORS. . . STROMAL CELLS AND OSTEOCLAST PROGENTYORS. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 EEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                            -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED
A NUMBER OF OTHER HEMATOPOLETIC AND IMMUNE ORGANS. NOT DETECTED
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRP-CDPVMGL 83
                                                                                                                                                                                                                                      -1- SIMILARITY: CONTAINS LANGER/THER-TYPE CYSTEINE-RICH REGION.
EMBL; AB002146; BAA32010.1; -.
EMBL; AB00822; BAA32076.1; -.
EMBL; AB00821; BAA32076.1; -.
EMBL; AB00821; BAA32076.1; -.
EMBL; AB0821; ABA32076.1; -.
EMBL; CONTAINS ABS3709.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 KAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTCKNPLE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> D (IN REF. 2 AND 3). EB42FA51C9D7C71E CRC64;
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N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSTEOPROTEGERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00652; TITE, NGFR_1; UNKNOWN_1.
PROSITE; PS00505; TNFR_NGFR_2; 2.
Glycoprotein; Repeat; Cytokine; Signal.
SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
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SMART; SM00208; TNFR; 4.
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                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
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                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20111091; PubMed=10642582;
Bobe J., Goetz F.W.;
"A tumor necrosis factor decoy receptor homologue is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Gaps
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DECOY TNF RECEPTOR.
Salvelinus fontinalis (Brook trout) (Brook char).
Salvelinus fontinalis (Brook trout) (Treibrelate) (Brook char).
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.0%; Score 238; DB 13; Length 302; 31.6%; Pred. No. 8e-18; ive 22; Mismatches 72; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AA; 34037 MW; E44C73477F05C3DF CRC64;
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                                                                                                                                                                                                                                                                                             Buol. Reprod. 62:420-426(2000).
EMBL; AF156738; AAD56428.1; -
INSEP; O14763; 1D4V.
INTERPROD. IPROD0561; BGF-11ke.
INTERPROD. IPROD1368; TNFR_C6.
Friam. PF000203; TNFR_C6; 1.
SWART; SW00208; TNFR; 4.
PROSITE; PS00186; EGF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
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Best Local Similarity 31.64
Matches 50; Conservative
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